

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: July 26, 2004, 15:26:55 ; Search time 1325 Seconds
(without alignments)
2257.109 Million cell updates/sec

Title: US-09-719-533a-1_COPY_527_595

Perfect score: 69

Sequence: 1 ACAACTCTGCTCAGGAAC.....AACCTACGACAGAACTGC 69

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl:

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3: gb_in.*
4: gb_om.*
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10: gb_ro.*
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39: em_htgo_hum.*
40: em_htgo_mus.*
41: em_htgo_other.*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	69	100.0	192	14	AF198767	AF198767 Hepatitis
2	69	100.0	3215	6	BD232230	BD232230 Hepatitis
3	67.4	97.7	192	14	AF198698	AF198698 Hepatitis
4	67.4	97.7	192	14	AF198704	AF198704 Hepatitis
5	67.4	97.7	192	14	AF198705	AF198705 Hepatitis
6	67.4	97.7	192	14	AF198706	AF198706 Hepatitis
7	67.4	97.7	192	14	AF198707	AF198707 Hepatitis
8	67.4	97.7	192	14	AF198708	AF198708 Hepatitis
9	67.4	97.7	192	14	AF198709	AF198709 Hepatitis
10	67.4	97.7	192	14	AF198710	AF198710 Hepatitis
11	67.4	97.7	192	14	AF198711	AF198711 Hepatitis
12	67.4	97.7	192	14	AF198712	AF198712 Hepatitis
13	67.4	97.7	192	14	AF198713	AF198713 Hepatitis
14	67.4	97.7	192	14	AF198714	AF198714 Hepatitis
15	67.4	97.7	192	14	AF198715	AF198715 Hepatitis
16	67.4	97.7	192	14	AF198716	AF198716 Hepatitis
17	67.4	97.7	192	14	AF198717	AF198717 Hepatitis
18	67.4	97.7	192	14	AF198718	AF198718 Hepatitis
19	67.4	97.7	192	14	AF198721	AF198721 Hepatitis
20	67.4	97.7	192	14	AF198722	AF198722 Hepatitis
21	67.4	97.7	192	14	AF198723	AF198723 Hepatitis
22	67.4	97.7	192	14	AF198724	AF198724 Hepatitis
23	67.4	97.7	192	14	AF198725	AF198725 Hepatitis
24	67.4	97.7	192	14	AF198726	AF198726 Hepatitis
25	67.4	97.7	192	14	AF198727	AF198727 Hepatitis
26	67.4	97.7	192	14	AF198734	AF198734 Hepatitis
27	67.4	97.7	192	14	AF198735	AF198735 Hepatitis
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29	67.4	97.7	192	14	AF198737	AF198737 Hepatitis
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31	67.4	97.7	192	14	AF198739	AF198739 Hepatitis
32	67.4	97.7	192	14	AF198740	AF198740 Hepatitis
33	67.4	97.7	192	14	AF198741	AF198741 Hepatitis
34	67.4	97.7	192	14	AF198742	AF198742 Hepatitis
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36	67.4	97.7	192	14	AF198744	AF198744 Hepatitis
37	67.4	97.7	192	14	AF198745	AF198745 Hepatitis
38	67.4	97.7	192	14	AF198746	AF198746 Hepatitis
39	67.4	97.7	192	14	AF198747	AF198747 Hepatitis
40	67.4	97.7	192	14	AF198748	AF198748 Hepatitis
41	67.4	97.7	192	14	AF198749	AF198749 Hepatitis
42	67.4	97.7	192	14	AF198750	AF198750 Hepatitis
43	67.4	97.7	192	14	AF198751	AF198751 Hepatitis
44	67.4	97.7	192	14	AF198752	AF198752 Hepatitis
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ALIGNMENTS

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DEFINITION Hepatitis B virus isolate CCN41 surface antigen gene, partial cds.
ACCESSION AF198767
VERSION AF198767.1 GI:8537407
KEYWORDS
SOURCE
ORGANISM Hepatitis B virus
Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
REFERENCE 1 (bases 1 to 192)
AUTHORS Xia,G.-L., Nainan,O.V., Jia,Z.-Y., Cao,H.-L., Liu,C.-B. and Margolis,H.S.
TITLE Distribution of hepatitis B virus subtypes and genotypes in China
JOURNAL Unpublished


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LOCUS AF198704 192 bp DNA linear VRL 08-DEC-1999
DEFINITION Hepatitis B virus isolate CCC57 surface antigen gene, partial cds.
ACCESSION AF198704
VERSION AF198704.1 GI:6537344
SOURCE
ORGANISM Hepatitis B virus
VIRUSES; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
REFERENCE 1 (bases 1 to 192)
AUTHORS Xia,G.-L., Nainan,O.V., Jia,Z.-Y., Cao,H.-L., Liu,C.-B. and Margolis,H.S.
TITLE Distribution of hepatitis B virus subtypes and genotypes in China
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 192)
AUTHORS Xia,G.-L., Nainan,O.V., Jia,Z.-Y., Cao,H.-L., Liu,C.-B. and Margolis,H.S.
TITLE Direct Submission
JOURNAL Submitted (26-OCT-1999) Division of Viral and Rickettsial Disease, National Center for Infectious Diseases, CDC, 1600 Clifton Road NE, MS-A33, Atlanta, GA 30333, USA
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Matches 68; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 61 AGAACTGC 69
Db 96 GGAACCTGC 104

RESULT 5
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LOCUS AF198705 192 bp DNA linear VRL 08-DEC-1999
DEFINITION Hepatitis B virus isolate CCC58 surface antigen gene, partial cds.
ACCESSION AF198705
VERSION AF198705.1 GI:6537345
SOURCE
ORGANISM Hepatitis B virus
VIRUSES; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
REFERENCE 1 (bases 1 to 192)
AUTHORS Xia,G.-L., Nainan,O.V., Jia,Z.-Y., Cao,H.-L., Liu,C.-B. and Margolis,H.S.
TITLE Distribution of hepatitis B virus subtypes and genotypes in China
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 192)
AUTHORS Xia,G.-L., Nainan,O.V., Jia,Z.-Y., Cao,H.-L., Liu,C.-B. and Margolis,H.S.
TITLE Direct Submission
JOURNAL Submitted (26-OCT-1999) Division of Viral and Rickettsial Disease, National Center for Infectious Diseases, CDC, 1600 Clifton Road NE, MS-A33, Atlanta, GA 30333, USA
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Matches 68; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ACAACTCTCTCAAGAACCTCTATGTTTCCCTCATGTTGCTGTACAAAACCTACGGAC 60
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QY 61 AGAACTGC 69
Db 96 GGAACCTGC 104

RESULT 6
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LOCUS AF198706 192 bp DNA linear VRL 08-DEC-1999
DEFINITION Hepatitis B virus isolate CCC59 surface antigen gene, partial cds.
ACCESSION AF198706
VERSION AF198706.1 GI:6537346
SOURCE
ORGANISM Hepatitis B virus
VIRUSES; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
REFERENCE 1 (bases 1 to 192)
AUTHORS Xia,G.-L., Nainan,O.V., Jia,Z.-Y., Cao,H.-L., Liu,C.-B. and Margolis,H.S.
TITLE Distribution of hepatitis B virus subtypes and genotypes in China
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 192)
AUTHORS Xia,G.-L., Nainan,O.V., Jia,Z.-Y., Cao,H.-L., Liu,C.-B. and Margolis,H.S.
TITLE Direct Submission
JOURNAL Submitted (26-OCT-1999) Division of Viral and Rickettsial Disease, National Center for Infectious Diseases, CDC, 1600 Clifton Road NE, MS-A33, Atlanta, GA 30333, USA
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QY 61 AGAACTGC 69
Db 96 GGAACCTGC 104
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Qy      61  AGAAACTGC 69
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Db      96  GGAACACTGC 104

RESULT 7
AF198707
LOCUS      AF198707      192 bp      DNA      linear      VRL 08-DEC-1999
DEFINITION Hepatitis B virus isolate CCC50 surface antigen gene, partial cds.
ACCESSION  AF198707
VERSION     AF198707.1  GI:6537347
KEYWORDS
SOURCE      Hepatitis B virus
ORGANISM    Hepatitis B virus
REFERENCE   1  (bases 1 to 192)
AUTHORS     Xia,G.-L., Nainan,O.V., Jia,Z.-Y., Cao,H.-L., Liu,C.-B. and
Margolis,H.S.
TITLE       Distribution of hepatitis B virus subtypes and genotypes in China
JOURNAL     Unpublished
REFERENCE   2  (bases 1 to 192)
AUTHORS     Xia,G.-L., Nainan,O.V., Jia,Z.-Y., Cao,H.-L., Liu,C.-B. and
Margolis,H.S.
DIRECT SUBMISSION
TITLE       Submitted (26-OCT-1999) Division of Viral and Rickettsial Disease,
NATIONAL CENTER FOR INFECTIOUS DISEASES, CDC, 1600 Clifton Road NE,
MS-A33, Atlanta, GA 30333, USA
LOCATION/QUALIFIERS
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Matches 68; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy      61  AGAAACTGC 69
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Db      96  GGAACACTGC 104

CDS

RESULT 8
AF198708
LOCUS      AF198708      192 bp      DNA      linear      VRL 08-DEC-1999
DEFINITION Hepatitis B virus isolate CCC55 surface antigen gene, partial cds.
ACCESSION  AF198708
VERSION     AF198708.1  GI:6537348
KEYWORDS
SOURCE      Hepatitis B virus
ORGANISM    Hepatitis B virus
REFERENCE   1  (bases 1 to 192)
AUTHORS     Xia,G.-L., Nainan,O.V., Jia,Z.-Y., Cao,H.-L., Liu,C.-B. and
Margolis,H.S.
TITLE       Distribution of hepatitis B virus subtypes and genotypes in China
JOURNAL     Unpublished
REFERENCE   2  (bases 1 to 192)
AUTHORS     Xia,G.-L., Nainan,O.V., Jia,Z.-Y., Cao,H.-L., Liu,C.-B. and
Margolis,H.S.
DIRECT SUBMISSION
TITLE       Submitted (26-OCT-1999) Division of Viral and Rickettsial Disease,
NATIONAL CENTER FOR INFECTIOUS DISEASES, CDC, 1600 Clifton Road NE,
MS-A33, Atlanta, GA 30333, USA
LOCATION/QUALIFIERS
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Query Match      97.7%; Score 67.4; DB 14; Length 192;
Best Local Similarity 98.6%; Pred. No. 1.7e-14;
Matches 68; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Db      96  GGAACACTGC 104

CDS

RESULT 9
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DEFINITION Hepatitis B virus isolate CCC60 surface antigen gene, partial cds.
ACCESSION  AF198709
VERSION     AF198709.1  GI:6537349
KEYWORDS
SOURCE      Hepatitis B virus
ORGANISM    Hepatitis B virus
REFERENCE   1  (bases 1 to 192)
AUTHORS     Xia,G.-L., Nainan,O.V., Jia,Z.-Y., Cao,H.-L., Liu,C.-B. and
Margolis,H.S.
TITLE       Distribution of hepatitis B virus subtypes and genotypes in China
JOURNAL     Unpublished
REFERENCE   2  (bases 1 to 192)
AUTHORS     Xia,G.-L., Nainan,O.V., Jia,Z.-Y., Cao,H.-L., Liu,C.-B. and
Margolis,H.S.
DIRECT SUBMISSION
TITLE       Submitted (26-OCT-1999) Division of Viral and Rickettsial Disease,
NATIONAL CENTER FOR INFECTIOUS DISEASES, CDC, 1600 Clifton Road NE,
MS-A33, Atlanta, GA 30333, USA
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Matches 68; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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TITLE       Distribution of hepatitis B virus subtypes and genotypes in China
JOURNAL     Unpublished
REFERENCE   2  (bases 1 to 192)
AUTHORS     Xia,G.-L., Nainan,O.V., Jia,Z.-Y., Cao,H.-L., Liu,C.-B. and
Margolis,H.S.
DIRECT SUBMISSION
TITLE       Submitted (26-OCT-1999) Division of Viral and Rickettsial Disease,
NATIONAL CENTER FOR INFECTIOUS DISEASES, CDC, 1600 Clifton Road NE,
MS-A33, Atlanta, GA 30333, USA
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Best Local Similarity 98.6%; Pred. No. 1.7e-14;
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Qy      61  AGAAACTGC 69
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Db      96  GGAACACTGC 104

CDS

RESULT 9
AF198709
LOCUS      AF198709      192 bp      DNA      linear      VRL 08-DEC-1999
DEFINITION Hepatitis B virus isolate CCC60 surface antigen gene, partial cds.
ACCESSION  AF198709
VERSION     AF198709.1  GI:6537349
KEYWORDS
SOURCE      Hepatitis B virus
ORGANISM    Hepatitis B virus
REFERENCE   1  (bases 1 to 192)
AUTHORS     Xia,G.-L., Nainan,O.V., Jia,Z.-Y., Cao,H.-L., Liu,C.-B. and
Margolis,H.S.
TITLE       Distribution of hepatitis B virus subtypes and genotypes in China
JOURNAL     Unpublished
REFERENCE   2  (bases 1 to 192)
AUTHORS     Xia,G.-L., Nainan,O.V., Jia,Z.-Y., Cao,H.-L., Liu,C.-B. and
Margolis,H.S.
DIRECT SUBMISSION
TITLE       Submitted (26-OCT-1999) Division of Viral and Rickettsial Disease,
NATIONAL CENTER FOR INFECTIOUS DISEASES, CDC, 1600 Clifton Road NE,
MS-A33, Atlanta, GA 30333, USA
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Query Match      97.7%; Score 67.4; DB 14; Length 192;
Best Local Similarity 98.6%; Pred. No. 1.7e-14;
Matches 68; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1  ACAAACCTGCTCAAGAACTCTATGTTCCCTCATGTTGCTGTACAAAACCTACGGAC 60
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Db      96  GGAACACTGC 104

CDS

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LOCUS	192 bp	DNA	linear	VRL 08-DEC-1999
RESULT 11				
AF198711				

Hepatitis B virus isolate CCC64 surface antigen gene, partial cds.

AF198711.1 GI:6537351

Hepatitis B virus
Hepatitis B virus
Viruses; Retroviridae; Orthohepadnaviridae.
1 (bases 1 to 192)
Xia, G.-L., Nainan, O.V., Jia, Z.-Y., Cao, H.-L., Liu, C.-B. and
Margolis, H.S.
Distribution of hepatitis B virus subtypes and genotypes in China
Unpublished
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61 AGAAACTGC 69
|||||
66 GGAAACTGC 104

AF198712 192 bp DNA linear VRL 08-DEC-1999
Hepatitis B virus isolate CCC70 surface antigen gene, partial cds.
AF198712
AF198712.1 GI:6537352

Hepatitis B virus
Hepatitis B virus
Viruses; Retroviridae; Orthohepadnavirus.
1 (bases 1 to 192)
Xia, G.-L., Nainan, O.V., Jia, Z.-Y., Cao, H.-L., Liu, C.-B. and
Margolis, H.S.
Distribution of hepatitis B virus subtypes and genotypes in China
Unpublished
Location/Qualifiers
2 (bases 1 to 192)
Xia, G.-L., Nainan, O.V., Jia, Z.-Y., Cao, H.-L., Liu, C.-B. and
Margolis, H.S.
Direct Submission
Submitted (26-OCT-1999) Division of Viral and Rickettsial Disease,
National Center for Infectious Diseases, CDC, 1600 Clifton Road NE,
MS-A33, Atlanta, GA 30333, USA
Location/Qualifiers
1. 192

JOURNAL Unpublished
REFERENCE 2 (bases 1 to 192)
AUTHORS Xia,G.-L., Nainan,O.V., Jia,Z.-Y., Cao,H.-L., Liu,C.-B. and Margolis,H.S.
TITLE Direct Submission
JOURNAL Submitted (26-OCT-1999) Division of Viral and Rickettsial Disease, National Center for Infectious Diseases, CDC, 1600 Clifton Road NE, MS-A33, Atlanta, GA 30333, USA
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/note="HBsAg"
/codon_start=3
/product="surface antigen"
/protein_id="AAF15634.1"
/db_xref="GI:6537636"
/translation="STTSTGPKCTCTTFAQGTSMFPSCCCTKPTDGNCTCIPSSWA
FAKYLMEWASVRFSLSL"
ORIGIN
Query Match 97.7%; Score 67.4; DS 14; Length 192;
Best Local Similarity 98.6%; Pred. No. 1.7e-14;
Matches 68; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 ACAACTCTGCTCAAGGAACCTCTATGTTCCCTCCTGTTGCTGACAAAACCTACGGAC 60
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
36 ACAACTCTGCTCAAGGAACCTCTATGTTCCCTCCTGTTGCTGACAAAACCTACGGAC 95
QY 61 AGAAACTGC 69
DB |||||||
96 GGAAACTGC 104

Search completed: July 26, 2004, 17:05:37
Job time : 1326 secs

Result No.	Score	Query		Length	DB	ID	Description
		Match	%				
1	69	100.0	3215	3	AA029453		Mutant he
2	67.4	97.7	687	2	AAQ098179		Hepatitis
3	67.4	97.7	690	2	AAQ098180		Hepatitis
4	65.8	95.4	297	4	AA056121		HBV DNA p
5	65.8	95.4	297	4	AA056122		HBV DNA p
6	65.8	95.4	297	4	AA056123		HBV DNA p
7	65.8	95.4	297	4	AA056120		HBV DNA p
8	65.8	95.4	297	4	AA056127		HBV DNA p
9	65.8	95.4	297	4	AA056128		HBV DNA p
10	65.8	95.4	306	9	AD044437		RNA virus
11	65.8	95.4	426	3	AA000819		Hepatitis
12	65.8	95.4	426	4	AA014305		Hepatitis
13	65.8	95.4	477	2	AA058385		Hepatitis
14	65.8	95.4	684	2	AAQ75318		Mutant He
15	64.2	93.0	426	3	AA000829		Hepatitis
16	64.2	93.0	426	4	AA014315		Hepatitis
17	62.6	90.7	3220	3	AA028924		Hepatitis
18	61	88.4	297	4	AA056108		HBV DNA p
19	61	88.4	297	4	AA056131		HBV DNA p
20	61	88.4	297	4	AA056126		HBV DNA p
21	61	88.4	297	4	AA056119		HBV DNA p
22	61	88.4	297	4	AA056124		HBV DNA p
23	61	88.4	297	4	AA056109		HBV DNA p

DR WPI; 2000-106103/09.
 DR P-PSDB; AAY44348, AAY44349, AAY44350, AAY44351.
 XX
 PT New vaccine-escape mutant of hepatitis B virus and related proteins,
 PT nucleic acids and antibodies, useful for diagnosis, prevention and
 PT treatment.
 XX
 PS Claim 3; Fig 3; 65pp; English.
 XX
 CC The present sequence encodes 4 overlapping reading frames of mutant human
 CC hepatitis B viral genome. This was isolated from a male, 11 year old
 CC Singaporean child which had received standard HBIG and HB vaccine and was
 CC infected with the mutated strain designated human hepatitis B virus
 CC surface antigen- 'S'- 145 Singapore strain, a year later. This DNA is
 CC used for recombinant production of mutant major surface antigen and as a
 CC source of diagnostic oligonucleotides. The mutated major surface antigen
 CC is used to raise specific antibodies, to identify specific binding agents
 CC and, in vaccines or compositions for treatment or prevention of HBV
 CC infection and hepatocellular carcinoma. Antibodies are used in diagnosis
 CC or for screening donated body fluids or tissues. (Updated on 06-AUG-2003
 CC to correct OS field.)
 XX
 SQ Sequence 3215 BP; 736 A; 852 C; 726 G; 901 T; 0 U; 0 Other;
 Query Match 100.0%; Score 69; DB 3; Length 3215;
 Best Local Similarity 100.0%; Pred. No. 1.9e-15;
 Matches 69; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ACAAACCTCTGCTCAAGGAACCTCTATGTTTCCCTCATGTTGCTGTACAAAACCTACGGAC 60
 DB 527 ACAAACCTCTGCTCAAGGAACCTCTATGTTTCCCTCATGTTGCTGTACAAAACCTACGGAC 586
 QY 61 AGAAACTGC 69
 DB 587 AGAAACTGC 595
 RESULT 2
 AAQ98179
 ID AAQ98179 standard; DNA; 687 BP.
 XX AC
 AC AAQ98179;
 XX
 DT 16-OCT-2003 (revised)
 DT 25-MAR-2003 (revised)
 DT 19-DEC-1995 (first entry)
 XX
 DE Hepatitis B virus surface antigen protein (mHBsAg) isolate 1.
 XX
 KW Hepatitis B virus; surface antigen; envelope region; 'a' determinant; ss.
 KW Hepatitis B virus; isolate 1.
 OS
 XX Key Location/Qualifiers
 FH variation 367..372
 FT /*tag= a
 FT /label= insertion
 XX
 PN WO9521189-A1.
 XX
 PD 10-AUG-1995.
 XX
 PF 02-FEB-1995; 95WO-GB000208.
 XX
 PR 02-FEB-1994; 94GB-00001987.
 XX
 PA (UNLO) IMPERIAL COLLEGE SCI TECHNOLOGY & MED.
 XX
 PI Karayiannis P, Thomas HC;
 DR WPI; 1995-283727/37.
 XX
 PT New mutant hepatitis B surface antigen - used for the detection

prevention and treatment of hepatitis B infection.
 Claim 10; Fig 6; 39pp; English.
 Two Chinese patients with hepatitis were studied. Patient No. 1 was a 58
 year old male, with a 6 year history of non-A, non-B chronic hepatitis.
 HBV-DNA was found by PCR in the absence of HBsAg and other HBV markers at
 a time when the patient had cirrhosis. Patient No. 2 was a 23 year old
 woman from the south of China who on routine testing had a slightly
 elevated serum aminotransferase (ALT) level and was positive for HBsAg
 and HBeAg, but negative for both immunoglobulin (Ig) M and IgG anti-HBs.
 On follow-up she continued to be HBV-DNA positive and was also anti-HB
 positive but negative for HBsAg, HBeAg and anti-HBs. Both patients were
 negative for hepatitis C virus (HVC) and HVC-RNA. DNA was isolated from
 serum samples and used as a template for PCR amplification. Primers M3
 and 3C (see AAQ98187 & AAQ98188) were used to amplify the Pre-C and C
 regions. Direct sequencing of the PCR products was carried out using
 sequencing primers AAQ98181-Q98186. The S genes consist of 687 bp in
 isolate 1, 690 bp in isolate 2 and 681 bp in the wild types. The S
 nucleotide and AA sequences of the mutants were compared with a published
 sequence of the same subtype (adv) and also with a wild type strain from
 an HBeAg-positive carrier from the same region. Sequencing results
 revealed an insertion in the S gene. Inserted sequences encode two
 additional AAs (Arg-Ala) between codons 122 and 123 in isolate 1, and
 three additional AAs (Arg-Gly-Ala) between codons 123 and 124 in isolate
 2. These insertions occur immediately before the 'a' determinant of
 HBsAg. (Updated on 25-MAR-2003 to correct PN field.) (Updated on 16-OCT-
 2003 to standardise OS field)
 SQ Sequence 687 BP; 139 A; 184 C; 144 G; 220 T; 0 U; 0 Other;
 Query Match 97.7%; Score 67.4; DB 2; Length 687;
 Best Local Similarity 98.6%; Pred. No. 4.8e-15;
 Matches 68; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 ACAAACCTCTGCTCAAGGAACCTCTATGTTTCCCTCATGTTGCTGTACAAAACCTACGGAC 60
 DB 379 ACAAACCTCTGCTCAAGGAACCTCTATGTTTCCCTCATGTTGCTGTACAAAACCTACGGAC 438
 QY 61 AGAAACTGC 69
 DB 439 GGAAACTGC 447
 RESULT 3
 AAQ98180
 ID AAQ98180 standard; DNA; 690 BP.
 XX AC
 AC AAQ98180;
 XX
 DT 16-OCT-2003 (revised)
 DT 25-MAR-2003 (revised)
 DT 19-DEC-1995 (first entry)
 XX
 DE Hepatitis B virus surface antigen protein (mHBsAg) isolate 2.
 XX
 KW Hepatitis B virus; surface antigen; envelope region; 'a' determinant; ss.
 KW Hepatitis B virus; isolate 2.
 OS
 XX Key Location/Qualifiers
 FH variation 368..376
 FT /*tag= a
 FT /label= insertion
 XX
 PN WO9521189-A1.
 XX
 PD 10-AUG-1995.
 XX
 PF 02-FEB-1995; 95WO-GB000208.
 XX
 PR 02-FEB-1994; 94GB-00001987.
 XX

(UNLO) IMPERIAL COLLEGE SCI TECHNOLOGY & MED.
Karayiannis P, Thomas HC;
WPI; 1995-283727/37.
New mutant hepatitis B surface antigen - used for the detection
prevention and treatment of hepatitis B infection.
Claim 10; Fig 7; 39pp; English.
Two Chinese patients with hepatitis were studied. Patient No. 1 was a 58
year old male, with a 6 year history of non-A, non-B chronic hepatitis.
HBV-DNA was found by PCR in the absence of HBeAg and other HBV markers at
a time when the patient had cirrhosis. Patient No. 2 was a 23 year old
woman from the south of China who on routine testing had a slightly
elevated serum aminotransferase (ALT) level and was positive for HBeAg
and HBeAg, but negative for both immunoglobulin (Ig) M and IgG anti-HBs.
On follow-up she continued to be HBV-DNA positive and was also anti-HB
positive but negative for HBeAg, HBeAg and anti-HBs. Both patients were
negative for hepatitis C virus (HVC) and HVC-RNA. DNA was isolated from
serum samples and used as a template for PCR amplification. Primers M3
and 3C (see AAQ98187 & AAQ98188) were used to amplify the Pre-C and C
regions. Direct sequencing of the PCR products was carried out using
sequencing primers AAQ98181-Q98186. The S genes consist of 687 bp in
isolate 1, 690 bp in isolate 2 and 681 bp in the wild types. The S
nucleotide and AA sequences of the mutants were compared with a published
sequence of the same subtype (adw) and also with a wild type strain from
an HBeAg-positive carrier from the same region. Sequencing results
revealed an insertion in the S gene. Inserted sequences encode two
additional AAs (Arg-Ala) between codons 122 and 123 in isolate 1, and
three additional AAs (Arg-Gly-Ala) between codons 123 and 124 in isolate
2. These insertions occur immediately before the 'a' determinant of
HBeAg. (Updated on 25-MAR-2003 to correct PN field.) (Updated on 16-OCT-
2003 to standardise OS field)
Sequence 690 BP; 140 A; 186 C; 145 G; 219 T; 0 U; 0 Other;
Query Match 97.7%; Score 67.4; DB 2; Length 690;
Best Local Similarity 98.6%; Pred. No. 4.8e-15;
Matches 68; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 ACAACTCTCTCAAGGAACCTCTATGTTCCCTCATGTTGCTGTACAAACCTACGGAC 60
DB 382 ACAACTCTCTCAAGGAACCTCTATGTTCCCTCATGTTGCTGTACAAACCTACGGAC 441
QY 61 AGAAACTGC 69
DB 442 GGAAACTGC 450
RESULT 4
AAF56121
ID AAF56121 standard; DNA; 297 BP.
AC AAF56121;
XX AAF56121;
XX 18-APR-2001 (first entry)
XX HBV DNA polymerase sequence genotype 3811.
XX HBV; hepatitis B virus; DNA polymerase gene; anti-HBV drug resistance;
XX mutation detection; ds.
XX Hepatitis B virus.
XX WO200104358-A2.
XX 18-JAN-2001.
XX 05-JUL-2000; 2000WO-EP006306.
XX 08-JUL-1999; 99EP-00870148.
XX Claim 16; Fig 1; 64pp; English.
PR 13-JUL-1999; 99US-0143546P.
XX (INNO-) INNOGENETICS NV.
XX Stuyver L, Maertens G, Van Geyt C;
XX WPI; 2001-138370/14.
XX Monitoring anti-HBV drug resistance by genetic detection of mutations in
DNA polymerase of HBV in patient's sample, involves hybridizing the
polynucleic acids of the sample with a probe and detecting the hybrid.
Claim 16; Fig 1; 64pp; English.
The present sequence is the sequence of the DNA polymerase gene from a
strain of hepatitis B virus (HBV). It is given in a specification
relating to a method for monitoring anti-HBV drug resistance in a patient
by genetic detection of any one of mutations L528M, M552V/I and/or
V/I/M555I in HBV DNA polymerase in a biological sample from the patient.
The method is useful in the field of genetic detection of anti-HBV drug
resistance during HBV therapy. The method is rapid, reliable and precise
Sequence 297 BP; 65 A; 81 C; 64 G; 87 T; 0 U; 0 Other;
Query Match 95.4%; Score 65.8; DB 4; Length 297;
Best Local Similarity 97.1%; Pred. No. 1.5e-14;
Matches 67; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 ACAACTCTCTCAAGGAACCTCTATGTTCCCTCATGTTGCTGTACAAACCTACGGAC 60
DB 50 ACAACTCTCTCAAGGAACCTCTATGTTCCCTCATGTTGCTGTACAAACCTACGGAC 109
QY 61 AGAAACTGC 69
DB 110 GGAAACTGC 118
RESULT 5
AAF56122
ID AAF56122 standard; DNA; 297 BP.
AC AAF56122;
XX AAF56122;
XX 18-APR-2001 (first entry).
XX HBV DNA polymerase sequence genotype 3774.
XX HBV; hepatitis B virus; DNA polymerase gene; anti-HBV drug resistance;
XX mutation detection; ds.
XX Hepatitis B virus.
XX WO200104358-A2.
XX 18-JAN-2001.
XX 05-JUL-2000; 2000WO-EP006306.
XX 08-JUL-1999; 99EP-00870148.
XX 13-JUL-1999; 99US-0143546P.
XX (INNO-) INNOGENETICS NV.
XX Stuyver L, Maertens G, Van Geyt C;
XX WPI; 2001-138370/14.
XX Monitoring anti-HBV drug resistance by genetic detection of mutations in
DNA polymerase of HBV in patient's sample, involves hybridizing the
polynucleic acids of the sample with a probe and detecting the hybrid.
Claim 16; Fig 1; 64pp; English.


```
XX 18-APR-2001 (first entry)
XX HBV DNA polymerase sequence genotype 4132.
DE
XX
XX HBV; hepatitis B virus; DNA polymerase gene; anti-HBV drug resistance;
KW mutation detection; ds.
XX
XX Hepatitis B virus.
OS
XX
XX WO200104358-A2.
PN
XX
XX 18-JAN-2001.
PD
XX
XX 05-JUL-2000; 2000WO-EP006306.
PF
XX
XX 08-JUL-1999; 99EP-00870148.
PR
XX 13-JUL-1999; 99US-0143546P.
PR
XX (INNO-) INNOGENETICS NV.
XX
XX Stuyver L, Maertens G, Van Geyt C;
PI WPI; 2001-138370/14.
DR
XX
XX Monitoring anti-HBV drug resistance by genetic detection of mutations in
PT DNA polymerase of HBV in patient's sample, involves hybridizing the
PT polynucleic acids of the sample with a probe and detecting the hybrid.
PT
XX
XX Claim 16; Fig 1; 64pp; English.
PS
XX
XX The present sequence is the sequence of the DNA polymerase gene from a
CC strain of hepatitis B virus (HBV). It is given in a specification
CC relating to a method for monitoring anti-HBV drug resistance in a patient
CC by genetic detection of any one of mutations L528M, M552V/I and/or
CC V/L/M551 in HBV DNA polymerase in a biological sample from the patient.
CC The method is useful in the field of genetic detection of anti-HBV drug
CC resistance during HBV therapy. The method is rapid, reliable and precise
CC
XX
XX Sequence 297 BP; 63 A; 82 C; 65 G; 87 T; 0 U; 0 Other;
SQ
Query Match 95.4%; Score 65.8; DB 4; Length 297;
Best Local Similarity 97.1%; Pred. No. 1.5e-14;
Matches 67; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ACAACTCCTGCTCAAGGAACCTCTATGTTTCCTCATGTTGCTGTACAAAACCTACGGAC 60
Db 50 ACGACTCCTGCTCAAGGAACCTCTATGTTTCCTCATGTTGCTGTACAAAACCTACGGAC 109
QY 61 AGAAACTGC 69
Db 110 GGAAACTGC 118

RESULT 9
AAF56128
ID AAF56128 standard; DNA; 297 BP.
XX
XX AAF56128;
AC
XX
XX 18-APR-2001 (first entry)
DT
XX
XX HBV DNA polymerase sequence genotype 4135.
DE
XX
XX HBV; hepatitis B virus; DNA polymerase gene; anti-HBV drug resistance;
KW mutation detection; ds.
XX
XX Hepatitis B virus.
OS
XX
XX WO200104358-A2.
PN
XX
XX 18-JAN-2001.
PD
XX
XX
```

```
PF 05-JUL-2000; 2000WO-EP006306.
XX
XX 08-JUL-1999; 99EP-00870148.
PR
XX 13-JUL-1999; 99US-0143546P.
XX
XX (INNO-) INNOGENETICS NV.
XX
XX Stuyver L, Maertens G, Van Geyt C;
PI WPI; 2001-138370/14.
DR
XX
XX Monitoring anti-HBV drug resistance by genetic detection of mutations in
PT DNA polymerase of HBV in patient's sample, involves hybridizing the
PT polynucleic acids of the sample with a probe and detecting the hybrid.
PT
XX
XX Claim 16; Fig 1; 64pp; English.
PS
XX
XX The present sequence is the sequence of the DNA polymerase gene from a
CC strain of hepatitis B virus (HBV). It is given in a specification
CC relating to a method for monitoring anti-HBV drug resistance in a patient
CC by genetic detection of any one of mutations L528M, M552V/I and/or
CC V/L/M551 in HBV DNA polymerase in a biological sample from the patient.
CC The method is useful in the field of genetic detection of anti-HBV drug
CC resistance during HBV therapy. The method is rapid, reliable and precise
CC
XX
XX Sequence 297 BP; 64 A; 83 C; 65 G; 85 T; 0 U; 0 Other;
SQ
Query Match 95.4%; Score 65.8; DB 4; Length 297;
Best Local Similarity 97.1%; Pred. No. 1.5e-14;
Matches 67; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ACAACTCCTGCTCAAGGAACCTCTATGTTTCCTCATGTTGCTGTACAAAACCTACGGAC 60
Db 50 ACGACTCCTGCTCAAGGAACCTCTATGTTTCCTCATGTTGCTGTACAAAACCTACGGAC 109
QY 61 AGAAACTGC 69
Db 110 GGAAACTGC 118

RESULT 10
ADD44437
ID ADD44437 standard; DNA; 306 BP.
XX
XX ADD44437;
AC
XX
XX 15-JAN-2004 (first entry)
DT
XX
XX RNA virus vector related HBV DNA #1.
DE
XX
XX genetic stability; foreign insert;
XX recombinant single-stranded RNA virus vector; mutagenesis; G/C content;
KW ds.
XX
XX Hepatitis B virus.
OS
XX
XX KR2002066048-A.
PN
XX
XX 14-AUG-2002.
PD
XX
XX 08-FEB-2001; 2001KR-00006229.
PF
XX
XX 08-FEB-2001; 2001KR-00006229.
PR
XX
XX (CREA-) CREAGENE INC.
PA
XX
XX Bae YS, Kim DY, Kim GT, Lee SG;
PI WPI; 2003-145037/14.
DR
XX
XX Improving genetic stability of a foreign insert nucleotide sequence in a
PT recombinant single-stranded RNA virus comprises performing a mutagenesis
PT of the foreign insert to provide even distribution of or to increase G/C
PT
```

PT content.
 XX Disclosure; SEQ ID NO 17; 24pp; Korean.
 XX
 CC The invention relates to a novel method for improving genetic stability
 CC of a foreign insert nucleotide sequence in a recombinant single-stranded
 CC RNA virus vector. The method comprises performing mutagenesis of a
 CC foreign insert nucleotide sequence to provide even distribution of G/C
 CC content throughout the overall foreign insert nucleotide sequence, and/or
 CC to increase G/C content of the foreign insert without causing amino acid
 CC substitutions. The method is useful in improving genetic stability of a
 CC foreign insert nucleotide sequence in a recombinant RNA virus. This
 CC polynucleotide sequence represents a virus DNA sequence relating to the
 CC recombinant single-stranded RNA virus vector of the invention.
 XX
 SQ Sequence 306 BP; 75 A; 85 C; 57 G; 89 T; 0 U; 0 Other;
 Query Match 95.4%; Score 65.8; DB 9; Length 306;
 Best Local Similarity 97.1%; Pred. No. 1.5e-14;
 Matches 67; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1 ACAACTCCTGCTCAAGGAACCTCTATGTTCCCTCATGTTGCTGTACAAAACCTACGGAC 60
 Db 199 ACAGCTCCTGCTCAAGGAACCTCTATGTTCCCTCATGTTGCTGTACAAAACCTACGGAC 258
 QY 61 AGAACTGC 69
 Db 259 GGAACTGC 267
 RESULT 11
 AAD00819
 ID AAD00819 standard; DNA; 426 BP.
 XX
 AC AAD00819;
 XX
 DT 15-SEP-2003 (revised)
 DT 04-OCT-2000 (first entry)
 XX
 DE Hepatitis B virus (HBV) 221499/HPBADW3 strain HBSAg encoding DNA.
 XX
 KW Hepatitis B surface antigen; HBSAg; Hepatitis B virus; HBV; vaccine;
 KW immunological profile; reference HBV; HBV polymerase; mutation;
 KW screening; treatment; prophylaxis; HBV infection; virucide; hepatotropic;
 KW antiinflammatory; ds.
 XX
 OS Hepatitis B virus; 221499/HPBADW3.
 XX
 FN WO200028009-A1.
 XX
 PD 18-MAY-2000.
 XX
 PF 10-NOV-1999; 99WO-AU0000993.
 XX
 PR 11-NOV-1998; 98AU-00007060.
 XX
 XX (NWHE-) NORTH WESTERN HEALTH CARE NETWORK.
 XX
 FI Locarnini SA, Torresi J, Earnest-Silveira L, Bartholomeusz AI;
 XX
 DR WPI; 2000-376527/32.
 XX
 FT Novel variant Hepatitis B virus and viral surface antigens exhibiting
 FT altered immunological profile useful for prophylaxis and treatment of
 FT Hepatitis B viral infection.
 XX
 PS Example 3; Fig 3; 70pp; English.
 XX
 CC The present sequence is the Hepatitis B virus (HBV) DNA of strain
 CC 221499/HPBADW3, encoding a portion of the surface antigen (HBSAg). The
 CC variant HBSAg comprises of single or multiple amino acid substitution,
 CC addition and/or deletion mutations, with an altered immunological
 CC profile, relative to an HBSAg from a reference HBV. These variants are

CC less susceptible to vaccines directed to the surface components and
 CC arises from selective immune pressure, following anti-HBV chemical
 CC therapy, aimed at disrupting HBV polymerase activity or function. Immune
 CC pressure may result from natural exposure to HBV or following vaccination
 CC with an avirulent or attenuated HBV or with a component of HBV. Variant
 CC HBV or HBSAg is useful for screening for an agent and for treatment or
 CC prophylaxis of HBV infection. These variants or recombinant polypeptides
 CC are also useful in biological compositions capable of inducing a
 CC neutralising immune response to the HBV variant. (Updated on 15-SEP-2003
 CC to standardise OS field)
 XX
 SQ Sequence 426 BP; 84 A; 112 C; 87 G; 143 T; 0 U; 0 Other;
 Query Match 95.4%; Score 65.8; DB 3; Length 426;
 Best Local Similarity 97.1%; Pred. No. 1.7e-14;
 Matches 67; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1 ACAACTCCTGCTCAAGGAACCTCTATGTTCCCTCATGTTGCTGTACAAAACCTACGGAC 60
 Db 118 ACGACTCCTGCTCAAGGAACCTCTATGTTCCCTCATGTTGCTGTACAAAACCTACGGAC 177
 QY 61 AGAACTGC 69
 Db 178 GGAACTGC 186
 RESULT 12
 AAD14305
 ID AAD14305 standard; DNA; 426 BP.
 XX
 AC AAD14305;
 XX
 DT 11-SEP-2003 (revised)
 DT 06-NOV-2001 (first entry)
 XX
 DE Hepatitis B virus (HBV) 221499/HPBADW3 strain HBSAg encoding DNA.
 XX
 KW Hepatitis B virus; HBV; altered sensitivity; agent; detection;
 KW Hepatitis B surface antigen; HBSAg; ss.
 XX
 OS Hepatitis B virus; 221499/HPBADW3.
 XX
 XX WO200157244-A1.
 XX
 PD 09-AUG-2001.
 XX
 PF 02-FEB-2001; 2001WO-AU0000098.
 XX
 PR 03-FEB-2000; 2000US-0179948P.
 XX
 PA (MELB-) MELBOURNE HEALTH.
 PA (PENN-) PENN STATE RES FOUND.
 XX
 PI Delaney W, Locarnini SA, Chen RYM, Bartholomeusz A, Isom H;
 XX
 DR WPI; 2001-496926/54.
 XX
 FT Detecting hepatitis B virus variant with altered sensitivity to agent,
 FT comprises infecting genetic construct containing replication competent
 FT genome to cells, contacting cells with agent and detecting replication of
 FT variant.
 XX
 PS Example 3; Fig 3; 110pp; English.
 XX
 CC The invention relates to a method of detecting variant hepatitis B virus
 CC (HBV) which exhibits altered sensitivity to agents. The method involves
 CC infecting a genetic construct containing a replication competent amount
 CC of the genome from variant HBV contained in or fused to a baculovirus
 CC genome; contacting cells with the agent to be tested; culturing cells
 CC under conditions sufficient for the variant HBV to replicate, express
 CC genetic sequences, and/or assemble, and/or release viral particles; and
 CC determining replication of variant HBV using viral-component-detection
 CC means. The method is useful for detecting variant HBV which exhibits

CC altered sensitivity to agents. The present sequence is the HBV DNA of
CC strain 221499/HBADM3, encoding a portion of the surface antigen (HBSAg).
CC (Updated on 11-SEP-2003 to standardise OS field)

CC Sequence 426 BP; 84 A; 112 C; 87 G; 143 T; 0 U; 0 Other;

Query Match 95.4%; Score 65.8; DB 4; Length 426;
Best Local Similarity 97.1%; Pred. No. 1.7e-14;
Matches 67; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ACAACTCTGCTCAAGGAACCTCTATGTTTCCCTCATGTTCTGTACAAAACCTACGGAC 60
Db 118 ACCACTCTCTCTCAAGGAACCTCTATGTTTCCCTCATGTTCTGTACAAAACCTACGGAC 177

QY 61 AGAAACTGC 69
Db 178 GGAAACTGC 186

RESULT 13

AAAT58385
ID AAT58385 standard; DNA; 477 BP.

XX
AC AAT58385;

DT 04-AUG-1997 (first entry)

XX Hepatitis B virus target sequence (map positions 236-712).

XX detection; primer; set; amplicon; threshold concentration; probe;
KW ligase chain reaction; LCR; bacteria; virus; HIV; PCR; amplify;
KW Chlamydia trachomatis; ds.

XX Hepatitis B virus.

XX WO9636736-A2.

XX 21-NOV-1996.

XX 17-MAY-1996; 96WO-US007138.

XX 19-MAY-1995; 95US-00444615.

XX (ABBO) ABBOTT LAB.

XX Solomon NA, Bouma SR;

XX WPI; 1997-012104/01.

XX Detection of target nucleic acid sequences - using different primer sets
PT capable of producing detectable amplicons at different threshold concns.

XX Example 2; Page 29; 46pp; English.

XX Determining approximate amounts of target nucleic acid sequences in a
CC sample comprises contacting the sample with an amplification reaction
CC mixture comprising 2 (different) primer sets which react with 2
CC (different) sub-target regions of the target sequence, the sets being
CC selected such that they are capable of producing a detectable amplicon
CC only at or above a certain threshold concn. of the target sequence, the
CC threshold concns. being different for each primer set. The reaction
CC mixture is subjected to amplification conditions sufficient to produce a
CC detectable amplicon from at least one of the primer sets when the test
CC sample contains a concn. of target sequence which is at or above the
CC threshold concn. at which the primer set is capable of producing a
CC detectable amplicon. The reaction mixture is analysed to determine
CC whether an amplicon was produced in the reaction mixture from at least
CC one primer set so as to determine whether the test sample contains a
CC concn. of target sequence at or above the threshold concn. corresponding
CC to at least one primer. The method can be used for the detection of
CC targets such as bacteria or viruses, e.g. HIV or Chlamydia trachomatis.
CC The method can provide for the detection of a relative or approximate
CC amt. of a target sequence in a test sample without requiring extensive

CC sample manipulation or preparation. Simultaneous PCR of two separate sub-
CC target regions of an Hepatitis B Virus (HBV) target sequence was
CC performed using two primer sets which have widely differing
CC sensitivities. The present sequence comprises the first sub-target
CC sequence corresponding to map positions 236-712 of HBV. AAT58387-88
CC comprise the primer set for this target sequence

SQ Sequence 477 BP; 96 A; 135 C; 96 G; 150 T; 0 U; 0 Other;

Query Match 95.4%; Score 65.8; DB 2; Length 477;

Best Local Similarity 97.1%; Pred. No. 1.7e-14;

Matches 67; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ACAACTCTGCTCAAGGAACCTCTATGTTTCCCTCATGTTCTGTACAAAACCTACGGAC 60

Db 292 ACAACTCTGCTCAAGGAACCTCTATGTTTCCCTCATGTTCTGTACAAAACCTACGGAT 351

QY 61 AGAAACTGC 69

Db 352 GGAAACTGC 360

RESULT 14

AAQ75318
ID AAQ75318 standard; DNA; 684 BP.

XX
AC AAQ75318;

DT 25-MAR-2003 (revised)

DT 22-SEP-1995 (first entry)

XX Mutant Hepatitis B virus nucleic acid sequence.

XX Hepatitis B virus; HBV; mutant; detection; surface antigen; HBSAg;
KW detection; vaccine; diagnostic; prognosis; therapy; ss.

XX Hepatitis B virus.

FT Key Location/Qualifiers
FT misc_difference 185..187

FT /tag= a

FT /transl_except= AAC encodes Threonine.

FT misc_difference 289..291

FT /tag= b

FT /transl_except= CCT encodes Leucine.

FT insertion_seq 367..372

FT /tag= c

PN WO9426904-A1.

PD 24-NOV-1994.

PF 09-MAY-1994; 94WO-US005090.

XX 07-MAY-1993; 93US-00059031.

XX (ABBO) ABBOTT LAB.

XX (UNIU) UNIV GLASGOW.

XX Carman W, Decker RH, Wallace L, Mims LT, Solomon LR;

XX WPI; 1995-006799/01.

XX P-PSDB; AAR67368.

XX New mutant hepatitis B virus polynucleotide - used to develop prods. for
PT diagnosis, prognosis, therapy and studies involving hepatitis B
PT infection.

XX Example 2; Page 48-49; 59pp; English.

XX The mutant hepatitis B virus (HBV) polynucleotide comprises an insertion
CC of six nucleotides at position 366 of the HBV surface antigen (HBSAg)
CC gene. The polynucleotide can be used for detection of mutant HBV and for

CC the production of mutant polypeptides which can be used in vaccines for
CC the treatment of infection. Antibodies against such polypeptides can be
CC used for detecting the mutant HBV antigen. (Updated on 25-MAR-2003 to
CC correct PN field.)
XX
SQ Sequence 684 BP; 140 A; 189 C; 142 G; 213 T; 0 U; 0 Other;
Query Match 95.4%; Score 65.8; DB 2; Length 684;
Best Local Similarity 97.1%; Pred. No. 1.9e-14; Indels 0; Gaps 0;
Matches 67; Conservative 0; Mismatches 2;
QY 1 ACAACTCTCTCAAGGAACCTCTATGTTTCCCTCATGTTGCTGTACAAAACCTACGGAC 60
DB 379 ACGACTCTCTCAAGGAACCTCTATGTTTCCCTCATGTTGCTGTACAAAACCTACGGAC 438
QY 61 AGAAACTGC 69
DB 439 AGAAACTGC 447
RESULT 15
AD00829
ID AAD00829 standard; DNA; 426 BP.
XX
AC AAD00829;
XX
DT 15-SEP-2003 (revised)
DT 04-OCT-2000 (first entry)
DE Hepatitis B virus (HBV) 229417/HPBADW1 strain HBSAg encoding DNA.
XX
KW Hepatitis B surface antigen; HBSAg; Hepatitis B virus; HBV; vaccine;
KW immunological profile; reference HBV; HBV polymerase; mutation;
KW screening; treatment; prophylaxis; HBV infection; virucide; hepatotropic;
KW antiinflammatory; ds.
XX
OS Hepatitis B virus; 229417/HPBADW1.
XX
FN WO200028009-A1.
XX
PD 18-MAY-2000.
XX
PF 10-NOV-1999; 99WO-AU000993.
XX
PR 11-NOV-1998; 98AU-00007060.
XX
PA (NWHE-) NORTH WESTERN HEALTH CARE NETWORK.
XX
PI Locarnini SA, Torresi J, Earnest-Silveira L, Bartholomeusz AI;
XX
WPI; 2000-376527/32.
XX
Novel variant Hepatitis B virus and viral surface antigens exhibiting
altered immunological profile useful for prophylaxis and treatment of
Hepatitis B viral infection.
XX
Example 3; Fig 3; 70pp; English.
XX
The present sequence is the Hepatitis B virus (HBV) DNA of strain
229417/HPBADW1, encoding a portion of the surface antigen (HBSAg). The
variant HBSAg comprises of single or multiple amino acid substitution,
addition and/or deletion mutations, with an altered immunological
profile, relative to an HBSAg from a reference HBV. These variants are
less susceptible to vaccines directed to the surface components and
arises from selective immune pressure, following anti-HBV chemical
therapy, aimed at disrupting HBV polymerase activity or function. Immune
pressure may result from natural exposure to HBV or following vaccination
with an avirulent or attenuated HBV or with a component of HBV. Variant
HBV or HBSAg is useful for screening for an agent and for treatment or
prophylaxis of HBV infection. These variants or recombinant polypeptides
are also useful in biological compositions capable of inducing a
neutralising immune response to the HBV variant. (Updated on 15-SEP-2003
to standardise OS field)

XX
SQ Sequence 426 BP; 84 A; 110 C; 88 G; 144 T; 0 U; 0 Other;
Query Match 93.0%; Score 64.2; DB 3; Length 426;
Best Local Similarity 95.7%; Pred. No. 6.6e-14;
Matches 66; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 ACAACTCTCTCAAGGAACCTCTATGTTTCCCTCATGTTGCTGTACAAAACCTACGGAC 60
DB 118 ACAACTCTCTCAAGGAACCTCTATGTTTCCCTCATGTTGCTGTACAAAACCTATGGAT 177
QY 61 AGAAACTGC 69
DB 178 GGAAGACTGC 186
Search completed: July 26, 2004, 16:43:27
Job time : 201 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: July 26, 2004, 16:33:21 ; Search time 52 Seconds
(without alignments)
736.377 Million cell updates/sec

Title: US-09-719-533A-1_COPY_527_595

Perfect score: 69

Sequence: 1 ACAACTCTGCTCAAGAAC.....AACCTACGACAGAAACTGC 69

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents NA:*
1: /cgn2_6/prodata/2/ina/5A COMB.seq:*
2: /cgn2_6/prodata/2/ina/5B COMB.seq:*
3: /cgn2_6/prodata/2/ina/6A COMB.seq:*
4: /cgn2_6/prodata/2/ina/6B COMB.seq:*
5: /cgn2_6/prodata/2/ina/PCUS COMB.seq:*
6: /cgn2_6/prodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	67.4	97.7	687	2	US-08-500-914A-6
2	67.4	97.7	690	2	US-08-500-914A-8
3	65.8	95.4	477	2	US-08-697-404-11
4	65.8	95.4	681	2	US-08-500-914A-7
5	65.8	95.4	681	2	US-08-500-914A-9
6	65.8	95.4	684	1	US-08-447-591-1
7	65.8	95.4	684	1	US-08-450-943-1
8	65.8	95.4	684	1	US-08-059-031-1
9	65.8	95.4	684	2	US-08-450-942-1
10	65.8	95.4	684	5	PCT-US94-05090-1
11	61	88.4	817	1	US-09-471-573A-1
12	61	88.4	817	1	US-08-378-011A-4
13	61	88.4	845	1	US-08-378-011A-2
14	61	88.4	846	6	5164485-1
15	61	88.4	1200	3	US-08-854-531-5
16	61	88.4	1200	5	PCT-US95-13552-5
17	61	88.4	1286	4	US-10-133-907-3
18	59.4	86.1	550	4	US-09-306-420C-17
19	59.4	86.1	550	4	US-09-306-420C-19
20	59.4	86.1	585	3	US-08-075-520A-27
21	59.4	86.1	846	4	US-09-247-890-9
22	59.4	86.1	846	4	US-09-724-969-9
23	59.4	86.1	846	4	US-09-724-852-9
24	59.4	86.1	893	2	US-08-500-914A-1
25	59.4	86.1	1382	5	PCT-US92-07982A-1
26	59.4	86.1	3215	4	US-09-719-528A-1
27	59.4	86.1	3220	6	5196194-11

28	59.4	86.1	3220	6	5196194-15
29	59.4	86.1	3221	2	US-08-715-808-1
30	59.4	86.1	3504	2	US-08-760-797A-2
31	59.4	86.1	3504	2	US-08-760-797A-4
32	59.4	86.1	3504	3	US-08-932-929B-2
33	59.4	86.1	3504	3	US-08-932-929B-4
34	59.4	86.1	6371	2	US-08-715-808-5
35	59.4	86.1	6371	2	US-08-715-808-12
36	59.4	86.1	6375	2	US-08-715-808-14
37	59.4	86.1	7463	2	US-08-715-808-13
38	59.4	86.1	9325	2	US-08-715-808-2
39	59.4	86.1	9859	2	US-08-715-808-6
40	54.8	79.4	678	3	US-08-075-520A-26
41	54.8	79.4	681	5	PCT-US96-10602-13
42	54.8	79.4	801	4	US-09-311-784A-15
43	54.8	79.4	822	3	US-08-075-520A-14
44	54.8	79.4	846	4	US-03-247-890-11
45	54.8	79.4	846	4	US-09-724-969-11

ALIGNMENTS

RESULT 1

US-08-500-914A-6
; Sequence 6, Application US/08500914A
; Patent No. 5856084
; GENERAL INFORMATION:
; APPLICANT: KARAVIANIS, PETER
; APPLICANT: THOMAS, HOWARD C.
; TITLE OF INVENTION: HEPATITIS B VACCINE
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHYE P.C.
; STREET: 1100 NORTH GLEBE ROAD, 8TH FLOOR
; CITY: ARLINGTON
; STATE: VIRGINIA
; COUNTRY: U.S.A.
; ZIP: 22201-4714
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/500,914A
; FILING DATE: 28-DEC-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: MITCHELL, LEONARD C.
; REGISTRATION NUMBER: 29,009
; REFERENCE/DOCKET NUMBER: 1208-17
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-816-4000
; TELEFAX: 703-816-4100
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 687 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-500-914A-6

Query Match 97.7%; Score 67.4; DB 2; Length 687;
Best Local Similarity 98.6%; Pred. No. 1.2e-16;
Matches 68; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ACAACTCTGCTCAAGAACCTCTATGTTCCCTCATGTTGCTGTACAAACCTACCGAC 60

DB 379 ACAACTCTGCTCAAGAACCTCTATGTTCCCTCATGTTGCTGTACAAACCTACCGAC 438

QY 61 AGAAACTGC 69

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Db          439 GGAAGCTGC 447
|||||
RESULT 2
US-08-500-914A-8
; Sequence 8, Application US/08500914A
; Patent No. 5856084
; GENERAL INFORMATION:
; APPLICANT: KARAYIANNIS, PETER
; APPLICANT: THOMAS, HOWARD C.
; TITLE OF INVENTION: HEPATITIS B VACCINE
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHYE P.C.
; STREET: 1100 NORTH GLEBE ROAD, 8TH FLOOR
; CITY: ARLINGTON
; STATE: VIRGINIA
; COUNTRY: U.S.A.
; ZIP: 22201-4714
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/500,914A
; FILING DATE: 28-DEC-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: MITCHARD, LEONARD C.
; REGISTRATION NUMBER: 29,009
; REFERENCE/DOCKET NUMBER: 1208-17
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-816-4000
; TELEFAX: 703-816-4100
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 690 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-500-914A-8
Query Match          97.7%; Score 67.4; DB 2; Length 690;
Best Local Similarity 98.6%; Pred. No. 1.2e-16;
Matches 68; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy          1 ACAACTCTGCTCAAGAACTCTATGTTCCCTCATGTTGCTGTACAAAACCTACGGAC 60
Db          382 ACAACTCTGCTCAAGAACTCTATGTTCCCTCATGTTGCTGTACAAAACCTACGGAC 441
|||||
Qy          61 AGAAACTGC 69
Db          442 GGAAGCTGC 450
|||||
RESULT 3
US-08-697-404-11
; Sequence 11, Application US/08697404
; Patent No. 5858732
; GENERAL INFORMATION:
; APPLICANT: N. A. Solomon
; APPLICANT: S. R. Bouna
; TITLE OF INVENTION: WIDE DYNAMIC RANGE NUCLEIC ACID
; TITLE OF INVENTION: DETECTION USING AN AGGREGATE
; TITLE OF INVENTION: PRIMER SERIES
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Abbott Laboratories
; STREET: 100 Abbott Park Road
; CITY: Abbott Park
; STATE: ILLINOIS
; COUNTRY: U.S.A.
; ZIP: 60064-3500
; MEDIUM TYPE: Floppy disk
; COMPUTER: Macintosh
; OPERATING SYSTEM: System 7.0.1
; SOFTWARE: Microsoft Word 5.1a
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/697,404
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/444,615A
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Paul D. Yagser
; REGISTRATION NUMBER: 37,477
; REFERENCE/DOCKET NUMBER: 5692.US.01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 708/937-2341
; TELEFAX: 708/938-2623
; TELEX:
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 477 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: genomic DNA (HBV)
US-08-697-404-11
Query Match          95.4%; Score 65.8; DB 2; Length 477;
Best Local Similarity 97.1%; Pred. No. 4.4e-16;
Matches 67; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy          1 ACAACTCTGCTCAAGAACTCTATGTTCCCTCATGTTGCTGTACAAAACCTACGGAC 60
Db          292 ACAACTCTGCTCAAGAACTCTATGTTCCCTCATGTTGCTGTACAAAACCTACGGAT 351
|||||
Qy          61 AGAAACTGC 69
Db          352 GGAAGCTGC 360
|||||
RESULT 4
US-08-500-914A-7
; Sequence 7, Application US/08500914A
; Patent No. 5856084
; GENERAL INFORMATION:
; APPLICANT: KARAYIANNIS, PETER
; APPLICANT: THOMAS, HOWARD C.
; TITLE OF INVENTION: HEPATITIS B VACCINE
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHYE P.C.
; STREET: 1100 NORTH GLEBE ROAD, 8TH FLOOR
; CITY: ARLINGTON
; STATE: VIRGINIA
; COUNTRY: U.S.A.
; ZIP: 22201-4714
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/500,914A
; FILING DATE: 28-DEC-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: MITCHARD, LEONARD C.
; REGISTRATION NUMBER: 29,009
```

REFERENCE/DOCKET NUMBER: 1208-17
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-816-4000
TELEFAX: 703-816-4100
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 681 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-500-914A-7

Query Match 95.4%; Score 65.8; DB 2; Length 681;
Best Local Similarity 97.1%; Pred. No. 5e-16; 2; Indels 0; Gaps 0;
Matches 67; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ACAACTCTGCTCAAGGAACCTCTATGTTCCCTCATGTTGCTGTACAAAACCTACGGAC 60
|||
Db 373 ACAGCTCTGCTCAAGGAACCTCTATGTTCCCTCATGTTGCTGTACAAAACCTACGGAC 432

QY 61 AGAAACTGC 69
|||
Db 433 GGAACCTGC 441

RESULT 5
US-08-500-914A-9
; Sequence 9, Application US/08500914A
; Patent No. 5856084
; GENERAL INFORMATION:
; APPLICANT: KARAYIANNIS, PETER
; APPLICANT: THOMAS, HOWARD C.
; TITLE OF INVENTION: HEPATITIS B VACCINE
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHYE P.C.
; STREET: 1100 NORTH GLEBE ROAD, 8TH FLOOR
; CITY: ARLINGTON
; STATE: VIRGINIA
; COUNTRY: U.S.A.
; ZIP: 22201-4714
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/500,914A
; FILING DATE: 28-DEC-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: MITCHARD, LEONARD C.
; REGISTRATION NUMBER: 29,009
; REFERENCE/DOCKET NUMBER: 1208-17
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-816-4000
; TELEFAX: 703-816-4100
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 681 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-500-914A-9

Query Match 95.4%; Score 65.8; DB 2; Length 681;
Best Local Similarity 97.1%; Pred. No. 5e-16; 2; Indels 0; Gaps 0;
Matches 67; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ACAACTCTGCTCAAGGAACCTCTATGTTCCCTCATGTTGCTGTACAAAACCTACGGAC 60
|||
Db 373 ACAGCTCTGCTCAAGGAACCTCTATGTTCCCTCATGTTGCTGTACAAAACCTACGGAC 432

Db 373 ACAGCTCTGCTCAAGGAACCTCTATGTTCCCTCATGTTGCTGTACAAAACCTACGGAC 432

QY 61 AGAAACTGC 69
|||
Db 433 GGAACCTGC 441

RESULT 6
US-08-447-591-1
; Sequence 1, Application US/08447591
; Patent No. 5591440
; GENERAL INFORMATION:
; APPLICANT: CARMAN, WILLIAM
; APPLICANT: DECKER, RICHARD H
; APPLICANT: WALLACE, LESLEY
; APPLICANT: MIMMS, LARRY T
; APPLICANT: SOLOMON, LARRY R
; TITLE OF INVENTION: HEPATITIS B VIRUS MUTANTS, REAGENTS AND METHODS FOR DETECTION
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ABBOTT LABORATORIES D377/AP6D
; STREET: ONE ABBOTT PARK ROAD
; CITY: ABBOTT PARK
; STATE: IL
; COUNTRY: USA
; ZIP: 60064-3500
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/447,591
; FILING DATE: 23-MAY-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/059,031
; FILING DATE: 07-MAY-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: POREMBSKI, PRISCILLA E.
; REGISTRATION NUMBER: 33,207
; REFERENCE/DOCKET NUMBER: 5347 US.01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 708-937-6365
; TELEFAX: 708-938-2623
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 684 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..684
US-08-447-591-1

Query Match 95.4%; Score 65.8; DB 1; Length 684;
Best Local Similarity 97.1%; Pred. No. 5e-16; 0; Mismatches 0; Gaps 0;
Matches 67; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ACAACTCTGCTCAAGGAACCTCTATGTTCCCTCATGTTGCTGTACAAAACCTACGGAC 60
|||
Db 379 ACAGCTCTGCTCAAGGAACCTCTATGTTCCCTCATGTTGCTGTACAAAACCTACGGAC 438

QY 61 AGAAACTGC 69
|||
Db 439 AGAAACTGC 447

RESULT 7
US-08-450-943-1
; Sequence 1, Application US/08450943

[illegible]


```
ATTORNEY/AGENT INFORMATION:
NAME: POREMBSKI, PRISCILLA E.
REGISTRATION NUMBER: 33,207
REFERENCE/DOCKET NUMBER: 5347.US.01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 708-937-6365
TELEFAX: 708-938-2623
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 684 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 1..684
US-08-450-942-1

Query Match 95.4%; Score 65.8; DB 2; Length 684;
Best Local Similarity 97.1%; Pred. No. 5e-16;
Matches 67; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ACAACTCCTGCTCAAGGAACCTCTATGTTCCCTCATGTTGCTGTACAAAACCTACGGAC 60
Db 379 ACGACTCCTGCTCAAGGAACCTCTATGTTCCCTCATGTTGCTGTACAAAACCTACGGAC 438

QY 61 AGAAACTGC 69
Db 439 AGAAACTGC 447

RESULT 10
PCT-US94-05090-1
Sequence 1. Application PC/TUS9405090
GENERAL INFORMATION:
APPLICANT: CARMAN, WILLIAM
APPLICANT: DECKER, RICHARD H
APPLICANT: WALLACE, LESLEY
APPLICANT: MINNS, LARRY T
APPLICANT: SOLOMON, LARRY R
TITLE OF INVENTION: HEPATITIS B VIRUS MUTANTS, REAGENTS AND METHODS FOR DETECTION
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: ABBOTT LABORATORIES D377/AP6D
STREET: ONE ABBOTT PARK ROAD
CITY: ABBOTT PARK
STATE: IL
COUNTRY: USA
ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/05090
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: POREMBSKI, PRISCILLA E.
REGISTRATION NUMBER: 33,207
REFERENCE/DOCKET NUMBER: 5347.US.01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 708-937-6365
TELEFAX: 708-938-2623
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 684 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
```

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FEATURE:
NAME/KEY: CDS
LOCATION: 1..684
PCT-US94-05090-1

Query Match 95.4%; Score 65.8; DB 5; Length 684;
Best Local Similarity 97.1%; Pred. No. 5e-16;
Matches 67; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ACAACTCCTGCTCAAGGAACCTCTATGTTCCCTCATGTTGCTGTACAAAACCTACGGAC 60
Db 379 ACGACTCCTGCTCAAGGAACCTCTATGTTCCCTCATGTTGCTGTACAAAACCTACGGAC 438

QY 61 AGAAACTGC 69
Db 439 AGAAACTGC 447

RESULT 11
US-09-471-573A-1
Sequence 1. Application US/09471573A
Patent No. 6551820
GENERAL INFORMATION:
APPLICANT: Mason, Hugh
APPLICANT: Thanavala, Yasmin
TITLE OF INVENTION: Expression of Immunogenic Hepatitis B Surface Antigens In Transge
FILE REFERENCE: 3121/1080
CURRENT APPLICATION NUMBER: US/09/471,573A
CURRENT FILING DATE: 1999-12-23
PRIOR APPLICATION NUMBER: 60/113,827
PRIOR FILING DATE: 1998-12-23
NUMBER OF SEQ ID NOS: 41
SOFTWARE: PatentIn version 3.0
SEQ ID NO 1
LENGTH: 681
TYPE: DNA
ORGANISM: Unknown
FEATURE:
OTHER INFORMATION: Hepatitis B surface antigen
NAME/KEY: misc feature
OTHER INFORMATION: Hepatitis B surface antigen
US-09-471-573A-1

Query Match 88.4%; Score 61; DB 4; Length 681;
Best Local Similarity 92.8%; Pred. No. 3.6e-14;
Matches 64; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 ACAACTCCTGCTCAAGGAACCTCTATGTTCCCTCATGTTGCTGTACAAAACCTACGGAC 60
Db 373 ACGATTCTGCTCAAGGAACCTCTATGTTCCCTCATGTTGCTGTACAAAACCTACGGAC 432

QY 61 AGAAACTGC 69
Db 433 AGAAACTGC 441

RESULT 12
US-08-378-011A-4
Sequence 4. Application US/08378011A
Patent No. 5693497
GENERAL INFORMATION:
APPLICANT: TAKAMIZAWA, Akihisa
APPLICANT: FUJITA, Hiroyuki
APPLICANT: MANABE, Sadao
APPLICANT: KATO, Masahiko
APPLICANT: OSAE, Juichiro
APPLICANT: YOSHIDA, Iwao
APPLICANT: KONOBE, Takeo
APPLICANT: TAKAKU, Keisuke
TITLE OF INVENTION: HEPATITIS B VIRUS ANTIGEN AND A PROCESS FOR
TITLE OF INVENTION: PRODUCING SAME
NUMBER OF SEQUENCES: 4
```

;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Armstrong, Westernman, Hattori, McLeLeland &
;; ADDRESSEE: Naughton
;; STREET: 1725 K St. N.W. Suite 1000
;; CITY: Washington
;; STATE: D.C.
;; COUNTRY: U.S.A.
;; ZIP: 20006
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Diskette, 3.5 in, 1.44Mb
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS, Version 5.0
;; SOFTWARE: ASCII, generated using Word Perfect, version 5.1
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/378,011A
;; FILING DATE: 25-JAN-1995
;; CLASSIFICATION: 435
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: JP 61-143412
;; FILING DATE: 18-JUN-1986
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/061,518
;; FILING DATE: 15-JUN-1987
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/902,494
;; FILING DATE: 23-JUN-1992
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Stevens-Smith, Theresa M.
;; REGISTRATION NUMBER: 36,281
;; REFERENCE/DOCKET NUMBER: 870602B
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (202) 659-2930
;; TELEFAX: (202) 887-0357
;; TELEX: 440142
;; INFORMATION FOR SEQ ID NO: 4:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 817 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: cdNA from genomic RNA
US-08-378-011A-4

Query Match 88.4%; Score 61; DB 1; Length 817;
Best Local Similarity 92.8%; Pred. No. 3.8e-14;
Matches 64; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
QY 1 ACAACTCCTGCTCAAGGAACCTCTATGTTCCCTCATGTTGCTGTACAAAACCTACGGAC 60
DB 512 ACGATTCTGCTCAAGGAACCTCTATGTTCCCTCTTGTGCTGTACAAAACCTTCGGAC 571
QY 61 AGAAACTGC 69
DB 572 GGAACACTGC 580

RESULT 13
US-08-378-011A-2
; Sequence 2, Application US/08378011A
; Patent No. 5693497
; GENERAL INFORMATION:
; APPLICANT: TAKAMIZAWA, Akihisa
; APPLICANT: FUJITA, Hiroyuki
; APPLICANT: MANABE, Sadao
; APPLICANT: KATO, Masahiko
; APPLICANT: OSAME, Juichiro
; APPLICANT: YOSHIDA, Iwao
; APPLICANT: KONOBE, Takeo
; APPLICANT: TAKAKU, Keisuke
; TITLE OF INVENTION: HEPATITIS B VIRUS ANTIGEN AND A PROCESS FOR
; TITLE OF INVENTION: PRODUCING SAME
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:

;; ADDRESSEE: Armstrong, Westernman, Hattori, McLeLeland &
;; ADDRESSEE: Naughton
;; STREET: 1725 K St. N.W. Suite 1000
;; CITY: Washington
;; STATE: D.C.
;; COUNTRY: U.S.A.
;; ZIP: 20006
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Diskette, 3.5 in, 1.44Mb
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS, Version 5.0
;; SOFTWARE: ASCII, generated using Word Perfect, version 5.1
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/378,011A
;; FILING DATE: 25-JAN-1995
;; CLASSIFICATION: 435
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: JP 61-143412
;; FILING DATE: 18-JUN-1986
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/061,518
;; FILING DATE: 15-JUN-1987
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/902,494
;; FILING DATE: 23-JUN-1992
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Stevens-Smith, Theresa M.
;; REGISTRATION NUMBER: 36,281
;; REFERENCE/DOCKET NUMBER: 870602B
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (202) 659-2930
;; TELEFAX: (202) 887-0357
;; TELEX: 440142
;; INFORMATION FOR SEQ ID NO: 2:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 845 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: cdNA from genomic RNA
US-08-378-011A-2

Query Match 88.4%; Score 61; DB 1; Length 845;
Best Local Similarity 92.8%; Pred. No. 3.9e-14;
Matches 64; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
QY 1 ACAACTCCTGCTCAAGGAACCTCTATGTTCCCTCATGTTTCCCTCATGTTGCTGTACAAAACCTACGGAC 60
DB 540 ACGATTCTGCTCAAGGAACCTCTATGTTCCCTCTTGTGCTGTACAAAACCTTCGGAC 599
QY 61 AGAAACTGC 69
DB 600 GGAACACTGC 608

RESULT 14
5164485-1
; Patent No. 5164485
; APPLICANT: FUJISAWA, YUKIO; ITOH, YASUAKI; NISHIMURA, OSAMU
; FUJII, TOMOKO
; TITLE OF INVENTION: MODIFIED HEPATITIS B VIRUS SURFACE
; ANTIGEN P31 AND PRODUCTION THEREOF
; NUMBER OF SEQUENCES: 23
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/547,948
; FILING DATE: 03-JUL-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 898,425
; FILING DATE: 20-AUG-1986
; SEQ ID NO: 1
; LENGTH: 846
5164485-1

Query Match 88.4%; Score 61; DB 6; Length 846;
Best Local Similarity 92.8%; Pred. No. 3.9e-14;
Matches 64; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 ACAACTCCTGCTCAAGAACCTCTATGTTCCCTCATGTTGCTGTACAAAACCTACGGAC 60
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Db 538 ACGATTCCTGCTCAAGAACCTCTATGTTCCCTCATGTTGCTGTACAAAACCTACGGAC 597
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QY 61 AGAAACTGC 69
|||
Db 598 GGAACCTGC 606
|||

RESULT 15

US-08-854-531-5
; Sequence 5, Application US/08854531
; Patent No. 6025341
; GENERAL INFORMATION:
; APPLICANT: Wands, Jack
; APPLICANT: Tokushige, Katsutoshi
; APPLICANT: Wakita, Takaji
; TITLE OF INVENTION: CHIMERIC HEPATITIS B/HEPATITIS C VIRUS VACCINE
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock, Washburn, Kurtz, Mackiewicz & No. 6025341ris
; STREET: One Liberty Place, 46th floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/854,531
; FILING DATE: Herewith
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Deluca, Mark
; REGISTRATION NUMBER: 33,229
; REFERENCE/DOCKET NUMBER: APOL-0214
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 568-3100
; TELEFAX: (215) 568-3439
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1200 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
US-08-854-531-5

Query Match 88.4%; Score 61; DB 3; Length 1200;
Best Local Similarity 92.8%; Pred. No. 4.4e-14;
Matches 64; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 ACAACTCCTGCTCAAGAACCTCTATGTTCCCTCATGTTGCTGTACAAAACCTACGGAC 60
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Db 895 ACGATTCCTGCTCAAGAACCTCTATGTTCCCTCATGTTGCTGTACAAAACCTACGGAC 954
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QY 61 AGAAACTGC 69
|||
Db 955 GGAACCTGC 963
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Search completed: July 26, 2004, 17:29:04
Job time : 53 secs

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OM nucleic - nucleic search, using sw model

Run on: July 26, 2004, 17:05:50 ; Search time 229 Seconds
(without alignments)
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Title: US-09-719-533A-1_COPY_527_595
Perfect score: 69
Sequence: 1 ACAACTCTGCTCAGGAC.....AACCTACGACAGAACTGC 69

Scoring table: IDENTIFY NUC
Gapop 10.0 , Gapext 1.0

Searched: 3216467 seqs, 2444149694 residues
Total number of hits satisfying chosen parameters: 6432934

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications NA.*
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2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq.*
3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq.*
4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq.*
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11: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq.*
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19: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	65.8	95.4	306	15	US-10-071-867-19
2	65.8	95.4	425	10	US-09-781-891D-10
3	65.8	95.4	3215	13	US-10-453-792-284
4	65.8	95.4	3215	13	US-10-453-792-285
5	65.8	95.4	3215	13	US-10-453-792-287
6	64.2	93.0	426	10	US-09-781-891D-20
7	64.2	93.0	3215	13	US-10-453-792-286
8	62.6	90.7	3215	13	US-10-453-792-299
9	62.6	90.7	3215	13	US-10-453-792-300
10	61	88.4	426	10	US-09-781-891D-16
11	61	88.4	426	10	US-09-781-891D-17
12	61	88.4	681	17	US-10-335-774-1
13	61	88.4	1203	13	US-10-411-037-45
14	61	88.4	1203	13	US-10-411-026-45

15	61	88.4	1203	17	US-10-410-962-45	Sequence 45, Appl
16	61	88.4	1203	17	US-10-411-043-45	Sequence 45, Appl
17	61	88.4	1203	17	US-10-410-930-45	Sequence 45, Appl
18	61	88.4	1203	17	US-10-410-997-45	Sequence 45, Appl
19	61	88.4	1203	17	US-10-411-012-45	Sequence 45, Appl
20	61	88.4	1203	17	US-10-287-994-45	Sequence 45, Appl
21	61	88.4	1286	15	US-10-132-829-3	Sequence 3, Appl
22	61	88.4	1286	15	US-10-136-819-1	Sequence 1, Appl
23	61	88.4	1286	15	US-10-133-907-3	Sequence 3, Appl
24	61	88.4	3188	13	US-10-453-792-293	Sequence 293, App
25	61	88.4	3213	13	US-10-453-792-288	Sequence 288, App
26	61	88.4	3213	13	US-10-453-792-289	Sequence 289, App
27	61	88.4	3214	13	US-10-453-792-294	Sequence 294, App
28	61	88.4	3215	13	US-10-453-792-290	Sequence 290, App
29	61	88.4	3215	13	US-10-453-792-292	Sequence 292, App
30	61	88.4	3215	13	US-10-453-792-296	Sequence 296, App
31	61	88.4	3215	13	US-10-453-792-297	Sequence 297, App
32	61	88.4	3215	13	US-10-453-792-297	Sequence 11, Appl
33	61	88.4	5130	9	US-09-897-006-9	Sequence 9, Appl
34	61	88.4	5130	10	US-09-897-511A-9	Sequence 9, Appl
35	61	88.4	5130	13	US-10-397-079-9	Sequence 4, Appl
36	59.4	86.1	182	9	US-09-821-877-4	Sequence 9, Appl
37	59.4	86.1	426	10	US-09-781-891D-9	Sequence 11, Appl
38	59.4	86.1	426	10	US-09-781-891D-11	Sequence 15, Appl
39	59.4	86.1	426	10	US-09-781-891D-15	Sequence 17, Appl
40	59.4	86.1	550	15	US-10-260-451-17	Sequence 19, Appl
41	59.4	86.1	550	15	US-10-260-451-19	Sequence 27, Appl
42	59.4	86.1	585	16	US-10-394-896-27	Sequence 3, Appl
43	59.4	86.1	681	9	US-09-821-877-3	Sequence 6, Appl
44	59.4	86.1	690	9	US-09-821-877-6	Sequence 7, Appl
45	59.4	86.1	690	9	US-09-821-877-7	

ALIGNMENTS

RESULT 1
US-10-071-867-19
; Sequence 19, Application US/10071867
; Publication No. US20030166267A1
; GENERAL INFORMATION:
; APPLICANT: CreaGene Inc.
; TITLE OF INVENTION: METHOD FOR IMPROVING GENETIC STABILITY OF FOREIGN INSERT
; FILE REFERENCE: CreaGene-USA-1
; CURRENT APPLICATION NUMBER: US/10/071.867
; CURRENT FILING DATE: 2002-02-08
; PRIOR APPLICATION NUMBER: KR 2001-6229
; PRIOR FILING DATE: 2001-02-08
; NUMBER OF SEQ ID NOS: 95
; SOFTWARE: KopatentIn 1.71
; SEQ ID NO 19
; LENGTH: 306
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: HBVCs
US-10-071-867-19

Query Match 95.4%; Score 65.8; DB 15; Length 306;
Best Local Similarity 97.1%; Pred. No. 2.1e-15;
Matches 67; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 ACAACTCTGCTCAAGGACCTCTATGTTCCCTCATGTTGCTGTACAAAACCTACGGAC 60
DB 199 ACAGTCTTCTGCTCAAGGACCTCTATGTTCCCTCATGTTGCTGTACAAAACCTACGGAC 258
QY 61 AGAAACTGC 69
DB 259 GGAACTGC 267

RESULT 2

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US-09-781-891D-10
; Sequence 10, Application US/09781891D
; Publication No. US20030096222A1
; GENERAL INFORMATION:
; APPLICANT: Delaney, William IV
; APPLICANT: Locarnini, Stephen Alister
; APPLICANT: Chen, Robert Yung Ming
; APPLICANT: Bartholomeusz, Angeline
; APPLICANT: Isom, Harriet
; TITLE OF INVENTION: An assay
; FILE REFERENCE: 2378750/ETH
; CURRENT APPLICATION NUMBER: US/09/781,891D
; CURRENT FILING DATE: 2001-02-02
; PRIOR FILING DATE: 2000-02-03
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 10
; LENGTH: 425
; TYPE: DNA
; ORGANISM: HBV
US-09-781-891D-10

Query Match          95.4%; Score 65.8; DB 10; Length 425;
Best Local Similarity 97.1%; Pred. No. 2.3e-15;
Matches 67; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ACAAACCTCTGCTCAAGAACCTCTATGTTCCCTCATGTTGCTGTACAAAACCTACGGAC 60
Db 118 ACGACTCCTGCTCAAGAACCTCTATGTTCCCTCATGTTGCTGTACAAAACCTACGGAC 177

QY 61 AGAAACTGC 69
Db 178 GGAACACTGC 186

RESULT 3
US-10-453-792-284
; Sequence 284, Application US/10453792
; Publication No. US20040029110A1
; GENERAL INFORMATION:
; APPLICANT: STUYVER, LIEVEN
; APPLICANT: ROSSAU, RUDI
; MAERTENS, GEERT
; TITLE OF INVENTION: METHOD FOR TYPING AND DETECTING HBV
; NUMBER OF SEQUENCES: 313
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHYE P.C.
; STREET: 1100 NORTH GLEBE ROAD
; CITY: ARLINGTON
; STATE: VIRGINIA
; COUNTRY: U.S.A.
; ZIP: 22201-4714
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/453,792
; FILING DATE: 04-Jun-2003
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/155,885A
; FILING DATE: 08-Oct-1998
; APPLICATION NUMBER: PCT/EP97/02002
; FILING DATE: 21-Apr-1997
; APPLICATION NUMBER: EP 96870053.4
; FILING DATE: 19-Apr-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: SADOFF, B.J.
; REGISTRATION NUMBER: 36,663
; REFERENCE/DOCKET NUMBER: 2551-5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 816-4000
; TELEFAX: (703) 816-4100
; INFORMATION FOR SEQ ID NO: 285:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3215 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
;
US-09-719-533a-1_copy_527_595.rnpb
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 816-4000
; TELEFAX: (703) 816-4100
; INFORMATION FOR SEQ ID NO: 284:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3215 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; SEQUENCE DESCRIPTION: SEQ ID NO: 284:
US-10-453-792-284

Query Match          95.4%; Score 65.8; DB 13; Length 3215;
Best Local Similarity 97.1%; Pred. No. 4.6e-15;
Matches 67; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ACAAACCTCTGCTCAAGAACCTCTATGTTCCCTCATGTTGCTGTACAAAACCTACGGAC 60
Db 529 ACGACTCCTGCTCAAGAACCTCTATGTTCCCTCATGTTGCTGTACAAAACCTACGGAC 588

QY 61 AGAAACTGC 69
Db 589 GGAACACTGC 597

RESULT 4
US-10-453-792-285
; Sequence 285, Application US/10453792
; Publication No. US20040029110A1
; GENERAL INFORMATION:
; APPLICANT: STUYVER, LIEVEN
; APPLICANT: ROSSAU, RUDI
; MAERTENS, GEERT
; TITLE OF INVENTION: METHOD FOR TYPING AND DETECTING HBV
; NUMBER OF SEQUENCES: 313
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHYE P.C.
; STREET: 1100 NORTH GLEBE ROAD
; CITY: ARLINGTON
; STATE: VIRGINIA
; COUNTRY: U.S.A.
; ZIP: 22201-4714
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/453,792
; FILING DATE: 04-Jun-2003
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/155,885A
; FILING DATE: 08-Oct-1998
; APPLICATION NUMBER: PCT/EP97/02002
; FILING DATE: 21-Apr-1997
; APPLICATION NUMBER: EP 96870053.4
; FILING DATE: 19-Apr-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: SADOFF, B.J.
; REGISTRATION NUMBER: 36,663
; REFERENCE/DOCKET NUMBER: 2551-5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 816-4000
; TELEFAX: (703) 816-4100
; INFORMATION FOR SEQ ID NO: 285:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3215 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single

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Best Local Similarity 97.1%; Pred. No. 4.6e-15;
Matches 67; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 ACAAACCTCTGCTCAAGGAACCTCTATGTTTCCCTCATGTTGCTGTACAAAACCTACGGAC 60
Db 529 ACAAACCTCTGCTCAAGGAACCTCTATGTTTCCCTCATGTTGCTGTACAAAACCTACGGAT 588
QY 61 AGAAACTGC 69
Db 589 GGAACACTGC 597
RESULT 6
US-09-781-891D-20
; Sequence 20, Application US/09781891D
; Publication No. US2003009622A1
; GENERAL INFORMATION:
; APPLICANT: Delaney, William IV
; APPLICANT: Locarnini, Stephen Alister
; APPLICANT: Chen, Robert Yung Ming
; APPLICANT: Bartholomeusz, Angeline
; APPLICANT: Isom, Harriet
; TITLE OF INVENTION: An assay
; FILE REFERENCE: 2378750/EJH
; CURRENT APPLICATION NUMBER: US/09/781,891D
; CURRENT FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 60/179,948
; PRIOR FILING DATE: 2000-02-03
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 20
; LENGTH: 426
; TYPE: DNA
; ORGANISM: HBV
US-09-781-891D-20
Query Match 93.0%; Score 64.2; DB 10; Length 426;
Best Local Similarity 95.7%; Pred. No. 9.9e-15;
Matches 66; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 ACAAACCTCTGCTCAAGGAACCTCTATGTTTCCCTCATGTTGCTGTACAAAACCTACGGAC 60
Db 118 ACAAACCTCTGCTCAAGGAACCTCTATGTTTCCCTCATGTTGCTGTACAAAACCTACGGAT 177
QY 61 AGAAACTGC 69
Db 178 GGAACACTGC 186
RESULT 7
US-10-453-792-286
; Sequence 286, Application US/10453792
; Publication No. US20040029110A1
; GENERAL INFORMATION:
; APPLICANT: STUYVER, LIEVEN
; APPLICANT: ROSSAU, RUDI
; APPLICANT: MAERTENS, GEERT
; TITLE OF INVENTION: METHOD FOR TYPING AND DETECTING HBV
; NUMBER OF SEQUENCES: 313
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHVE P.C.
; STREET: 1100 NORTH GLEBE ROAD
; CITY: ARLINGTON
; STATE: VIRGINIA
; COUNTRY: U.S.A.
; ZIP: 22201-4714
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/453,792
; FILING DATE: 04-Jun-2003
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/155,885A
; FILING DATE: 08-Oct-1998
; APPLICATION NUMBER: PCT/EP97/02002
; FILING DATE: 21-Apr-1997
; APPLICATION NUMBER: EP 96870053.4
; FILING DATE: 19-Apr-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: SADOFF, B.J.
; REGISTRATION NUMBER: 36,663
; REFERENCE/DOCKET NUMBER: 2551-5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 816-4000
; TELEFAX: (703) 816-4100
; INFORMATION FOR SEQ ID NO: 287:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3215 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; SEQUENCE DESCRIPTION: SEQ ID NO: 287:
US-10-453-792-287
Query Match 95.4%; Score 65.8; DB 13; Length 3215;

TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; SEQUENCE DESCRIPTION: SEQ ID NO: 285:
US-10-453-792-285
Query Match 95.4%; Score 65.8; DB 13; Length 3215;
Best Local Similarity 97.1%; Pred. No. 4.6e-15;
Matches 67; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 ACAAACCTCTGCTCAAGGAACCTCTATGTTTCCCTCATGTTGCTGTACAAAACCTACGGAC 60
Db 529 ACAAACCTCTGCTCAAGGAACCTCTATGTTTCCCTCATGTTGCTGTACAAAACCTACGGAT 588
QY 61 AGAAACTGC 69
Db 589 GGAACACTGC 597
RESULT 5
US-10-453-792-287
; Sequence 287, Application US/10453792
; Publication No. US20040029110A1
; GENERAL INFORMATION:
; APPLICANT: STUYVER, LIEVEN
; APPLICANT: ROSSAU, RUDI
; APPLICANT: MAERTENS, GEERT
; TITLE OF INVENTION: METHOD FOR TYPING AND DETECTING HBV
; NUMBER OF SEQUENCES: 313
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHVE P.C.
; STREET: 1100 NORTH GLEBE ROAD
; CITY: ARLINGTON
; STATE: VIRGINIA
; COUNTRY: U.S.A.
; ZIP: 22201-4714
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/453,792
; FILING DATE: 04-Jun-2003
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/155,885A
; FILING DATE: 08-Oct-1998
; APPLICATION NUMBER: PCT/EP97/02002
; FILING DATE: 21-Apr-1997
; APPLICATION NUMBER: EP 96870053.4
; FILING DATE: 19-Apr-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: SADOFF, B.J.
; REGISTRATION NUMBER: 36,663
; REFERENCE/DOCKET NUMBER: 2551-5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 816-4000
; TELEFAX: (703) 816-4100
; INFORMATION FOR SEQ ID NO: 287:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3215 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; SEQUENCE DESCRIPTION: SEQ ID NO: 287:
US-10-453-792-287
Query Match 95.4%; Score 65.8; DB 13; Length 3215;

;; FILING DATE: 04-Jun-2003
;; CLASSIFICATION: <Unknown>
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US/09/155,885A
;; FILING DATE: 08-Oct-1998
;; APPLICATION NUMBER: PCT/EP97/02002
;; FILING DATE: 21-Apr-1997
;; APPLICATION NUMBER: EP 96870053.4
;; FILING DATE: 19-Apr-1996
;; ATTORNEY/AGENT INFORMATION:
;; NAME: SADOFF, B.J.
;; REGISTRATION NUMBER: 36,663
;; REFERENCE/DOCKET NUMBER: 2551-5
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (703) 816-4000
;; TELEFAX: (703) 816-4100
;; INFORMATION FOR SEQ ID NO: 286:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 3215 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: DNA (genomic)
;; HYPOTHETICAL: NO
;; ANTI-SENSE: NO
;; SEQUENCE DESCRIPTION: SEQ ID NO: 286:
US-10-453-792-286

Query Match 93.08; Score 64.2; DB 13; Length 3215;
Best Local Similarity 95.7%; Pred. No. 1.9e-14;
Matches 66; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 ACAACTCTGCTCAAGGAACCTCTATGTTTCCCTCATGTTGCTGTACAAAACCTACGGAC 60
Db 529 ACAACTCTGCTCAAGGAACCTCTATGTTTCCCTCATGTTGCTGTACAAAACCTATGGAT 588
QY 61 AGAAACTGC 69
Db 589 GGAACCTGC 597

RESULT 8
US-10-453-792-299
; Sequence 299, Application US/10453792
; Publication No. US20040029110A1
; GENERAL INFORMATION:
; APPLICANT: STUYVER, LIEVEN
; ROSSAU, RUDI
; MAERTENS, GEERT
; TITLE OF INVENTION: METHOD FOR TYPING AND DETECTING HBV
; NUMBER OF SEQUENCES: 313
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHUYE P.C.
; STREET: 1100 NORTH GLEBE ROAD
; CITY: ARLINGTON
; STATE: VIRGINIA
; COUNTRY: U.S.A.
; ZIP: 22201-4714
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/453,792
; FILING DATE: 04-Jun-2003
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/155,885A
; FILING DATE: 08-Oct-1998
; APPLICATION NUMBER: PCT/EP97/02002
; FILING DATE: 21-Apr-1997
; APPLICATION NUMBER: EP 96870053.4

;; FILING DATE: 19-Apr-1996
;; ATTORNEY/AGENT INFORMATION:
;; NAME: SADOFF, B.J.
;; REGISTRATION NUMBER: 36,663
;; REFERENCE/DOCKET NUMBER: 2551-5
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (703) 816-4000
;; TELEFAX: (703) 816-4100
;; INFORMATION FOR SEQ ID NO: 299:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 3215 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: DNA (genomic)
;; HYPOTHETICAL: NO
;; ANTI-SENSE: NO
;; SEQUENCE DESCRIPTION: SEQ ID NO: 299:
US-10-453-792-299

Query Match 90.7%; Score 62.6; DB 13; Length 3215;
Best Local Similarity 94.2%; Pred. No. 8.2e-14;
Matches 65; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 ACAACTCTGCTCAAGGAACCTCTATGTTTCCCTCATGTTGCTGTACAAAACCTACGGAC 60
Db 529 ACGATTCTGCTCAAGGAACCTCTATGTTTCCCTCATGTTGCTGTACAAAACCTTCGAC 588
QY 61 AGAAACTGC 69
Db 589 GGAACCTGC 597

RESULT 9
US-10-453-792-300
; Sequence 300, Application US/10453792
; Publication No. US20040029110A1
; GENERAL INFORMATION:
; APPLICANT: STUYVER, LIEVEN
; ROSSAU, RUDI
; MAERTENS, GEERT
; TITLE OF INVENTION: METHOD FOR TYPING AND DETECTING HBV
; NUMBER OF SEQUENCES: 313
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHUYE P.C.
; STREET: 1100 NORTH GLEBE ROAD
; CITY: ARLINGTON
; STATE: VIRGINIA
; COUNTRY: U.S.A.
; ZIP: 22201-4714
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/453,792
; FILING DATE: 04-Jun-2003
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/155,885A
; FILING DATE: 08-Oct-1998
; APPLICATION NUMBER: PCT/EP97/02002
; FILING DATE: 21-Apr-1997
; APPLICATION NUMBER: EP 96870053.4
; FILING DATE: 19-Apr-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: SADOFF, B.J.
; REGISTRATION NUMBER: 36,663
; REFERENCE/DOCKET NUMBER: 2551-5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 816-4000
; TELEFAX: (703) 816-4100

INFORMATION FOR SEQ ID NO: 300:
SEQUENCE CHARACTERISTICS:
LENGTH: 3215 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
SEQUENCE DESCRIPTION: SEQ ID NO: 300:
US-10-453-792-300

Query Match 90.7%; Score 62.6; DB 13; Length 3215;
Best Local Similarity 94.2%; Pred. No. 8.2e-14;
Matches 65; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 ACAACTCTGCTCAAGAACCTCTATGTTCCCTCATGTTGCTGTACAAACCTACGGAC 60
DB 529 ACGATTCTGCTCAAGAACCTCTATGTTCCCTCATGTTGCTGTACAAACCTACGGAC 588
QY 61 AGAAACTGC 69
DB 589 GGAACCTGC 597

RESULT 10
US-09-781-891D-16
; Sequence 16, Application US/09781891D
; Publication No. US20030096222A1
; GENERAL INFORMATION:
; APPLICANT: Delaney, William IV
; APPLICANT: Locarnini, Stephen Alister
; APPLICANT: Chen, Robert Yung Ming
; APPLICANT: Bartholomeusz, Angeline
; APPLICANT: Isom, Harriet
; TITLE OF INVENTION: An assay
; FILE REFERENCE: 2378750/EJH
; CURRENT APPLICATION NUMBER: US/09/781,891D
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 60/179,948
; PRIOR FILING DATE: 2000-02-03
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 16
; LENGTH: 426
; TYPE: DNA
; ORGANISM: HBV
US-09-781-891D-16

Query Match 88.4%; Score 61; DB 10; Length 426;
Best Local Similarity 92.8%; Pred. No. 1.7e-13;
Matches 64; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 ACAACTCTGCTCAAGAACCTCTATGTTCCCTCATGTTGCTGTACAAACCTACGGAC 60
DB 118 ACGATTCTGCTCAAGAACCTCTATGTTCCCTCATGTTGCTGTACAAACCTACGGAC 177
QY 61 AGAAACTGC 69
DB 178 GGAACCTGC 186

RESULT 11
US-09-781-891D-17
; Sequence 17, Application US/09781891D
; Publication No. US20030096222A1
; GENERAL INFORMATION:
; APPLICANT: Delaney, William IV
; APPLICANT: Locarnini, Stephen Alister
; APPLICANT: Chen, Robert Yung Ming
; APPLICANT: Bartholomeusz, Angeline
; APPLICANT: Isom, Harriet
; TITLE OF INVENTION: An assay

FILE REFERENCE: 2378750/EJH
; CURRENT APPLICATION NUMBER: US/09/781,891D
; CURRENT FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 60/179,948
; PRIOR FILING DATE: 2000-02-03
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 17
; LENGTH: 426
; TYPE: DNA
; ORGANISM: HBV
US-09-781-891D-17

Query Match 88.4%; Score 61; DB 10; Length 426;
Best Local Similarity 92.8%; Pred. No. 1.7e-13;
Matches 64; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 ACAACTCTGCTCAAGAACCTCTATGTTCCCTCATGTTGCTGTACAAACCTACGGAC 60
DB 118 ACGATTCTGCTCAAGAACCTCTATGTTCCCTCATGTTGCTGTACAAACCTACGGAC 177
QY 61 AGAAACTGC 69
DB 178 GGAACCTGC 186

RESULT 12
US-10-335-774-1
; Sequence 1, Application US/10335774
; Publication No. US20040086530A1
; GENERAL INFORMATION:
; APPLICANT: Mason, Hugh S.
; APPLICANT: Thanavala, Yasemin
; TITLE OF INVENTION: Expression of Immunogenic Hepatitis B Surface Antigens In Transgenic Plants
; FILE REFERENCE: 3121/1083
; CURRENT APPLICATION NUMBER: US/10/335,774
; CURRENT FILING DATE: 2003-01-02
; PRIOR APPLICATION NUMBER: 60/113,827
; PRIOR FILING DATE: 1998-12-23
; PRIOR APPLICATION NUMBER: 09/471,573
; PRIOR FILING DATE: 1999-12-23
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
; LENGTH: 681
; TYPE: DNA
; ORGANISM: Hepatitis B virus
; NAME/KEY: misc feature
; OTHER INFORMATION: Hepatitis B surface antigen
US-10-335-774-1

Query Match 88.4%; Score 61; DB 17; Length 681;
Best Local Similarity 92.8%; Pred. No. 2e-13;
Matches 64; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 ACAACTCTGCTCAAGAACCTCTATGTTCCCTCATGTTGCTGTACAAACCTACGGAC 60
DB 373 ACGATTCTGCTCAAGAACCTCTATGTTCCCTCATGTTGCTGTACAAACCTACGGAC 432
QY 61 AGAAACTGC 69
DB 433 GGAACCTGC 441

RESULT 13
US-10-411-037-45
; Sequence 45, Application US/10411037
; Publication No. US2004004346A1
; GENERAL INFORMATION:
; APPLICANT: Neose Technologies, Inc.
; APPLICANT: DePrees, Shawn

; APPLICANT: Zopf, David
 ; APPLICANT: Bayer, Robert
 ; APPLICANT: Hakes, David
 ; APPLICANT: Chen, Xi
 ; APPLICANT: Bowe, Caryn
 ; TITLE OF INVENTION: ALPHA GALACTOSIDASE A: REMODELING AND GLYCOCONJUGATION OF ALPHA
 ; FILE REFERENCE: 040853-01-5082
 ; CURRENT APPLICATION NUMBER: US/10/411,037
 ; CURRENT FILING DATE: 2003-04-09
 ; PRIOR APPLICATION NUMBER: US 60/328,523
 ; PRIOR FILING DATE: 2001-10-10
 ; PRIOR APPLICATION NUMBER: US 60/344,692
 ; PRIOR FILING DATE: 2001-10-19
 ; PRIOR APPLICATION NUMBER: US 60/387,292
 ; PRIOR FILING DATE: 2002-06-07
 ; PRIOR APPLICATION NUMBER: US 60/391,777
 ; PRIOR FILING DATE: 2002-06-25
 ; PRIOR APPLICATION NUMBER: US 60/396,594
 ; PRIOR FILING DATE: 2002-07-17
 ; PRIOR APPLICATION NUMBER: US 60/404,249
 ; PRIOR FILING DATE: 2002-08-16
 ; PRIOR APPLICATION NUMBER: US 60/407,527
 ; PRIOR FILING DATE: 2002-08-28
 ; NUMBER OF SEQ ID NOS: 75
 ; SOFTWARE: PatentIn version 3.2
 ; SEQ ID NO 45
 ; LENGTH: 1203
 ; TYPE: DNA
 ; ORGANISM: Hepatitis B virus
 US-10-411-037-45

Query Match 88.4%; Score 61; DB 13; Length 1203;
 Best Local Similarity 92.8%; Pred. No. 2.5e-13;
 Matches 64; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 ACACTCTCTCTCAAGAACCTTATGTTTCCTCATGTTGCTGTACAAACCTACGGAC 60
 Db 895 ACGATTCCTCTCAAGAACCTTATGTTTCCTCATGTTGCTGTACAAACCTACGGAC 60
 QY 61 AGAAACTGC 69
 Db 955 GGAACCTGC 963

RESULT 14
 US-10-411-026-45
 ; Sequence 45, Application US/10411026
 ; Publication No. US20040063911A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Neose Technologies, Inc.
 ; APPLICANT: Defrees, Shawn
 ; APPLICANT: Zopf, David
 ; APPLICANT: Bayer, Robert
 ; APPLICANT: Hakes, David
 ; APPLICANT: Chen, Xi
 ; TITLE OF INVENTION: PROTEIN REMODELING METHODS AND PROTEINS/PEPTIDES PRODUCED BY THE
 ; FILE REFERENCE: 040853-01-5053
 ; CURRENT APPLICATION NUMBER: US/10/411,026
 ; CURRENT FILING DATE: 2003-04-09
 ; PRIOR APPLICATION NUMBER: US 60/328,523
 ; PRIOR FILING DATE: 2001-10-10
 ; PRIOR APPLICATION NUMBER: US 60/344,692
 ; PRIOR FILING DATE: 2001-10-19
 ; PRIOR APPLICATION NUMBER: US 60/387,292
 ; PRIOR FILING DATE: 2002-06-07
 ; PRIOR APPLICATION NUMBER: US 60/391,777
 ; PRIOR FILING DATE: 2002-06-25
 ; PRIOR APPLICATION NUMBER: US 60/396,594
 ; PRIOR FILING DATE: 2002-07-17
 ; PRIOR APPLICATION NUMBER: US 60/404,249
 ; PRIOR FILING DATE: 2002-08-16

; PRIOR APPLICATION NUMBER: US 60/407,527
 ; PRIOR FILING DATE: 2002-08-28
 ; NUMBER OF SEQ ID NOS: 75
 ; SOFTWARE: PatentIn version 3.2
 ; SEQ ID NO 45
 ; LENGTH: 1203
 ; TYPE: DNA
 ; ORGANISM: Hepatitis B virus
 US-10-411-026-45
 Query Match 88.4%; Score 61; DB 13; Length 1203;
 Best Local Similarity 92.8%; Pred. No. 2.5e-13;
 Matches 64; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 ACACTCTCTCTCAAGAACCTTATGTTTCCTCATGTTGCTGTACAAACCTACGGAC 60
 Db 895 ACGATTCCTCTCAAGAACCTTATGTTTCCTCATGTTGCTGTACAAACCTACGGAC 60
 QY 61 AGAAACTGC 69
 Db 955 GGAACCTGC 963

RESULT 15
 US-10-410-962-45
 ; Sequence 45, Application US/10410962
 ; Publication No. US20040077836A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Neose Technologies, Inc.
 ; APPLICANT: Defrees, Shawn
 ; APPLICANT: Zopf, David
 ; APPLICANT: Bayer, Robert
 ; APPLICANT: Hakes, David
 ; APPLICANT: Chen, Xi
 ; APPLICANT: Bowe, Caryn
 ; TITLE OF INVENTION: GRANULOCYTE COLONY STIMULATING FACTOR: REMODELING AND
 ; FILE REFERENCE: 040853-01-5054
 ; CURRENT APPLICATION NUMBER: US/10/410,962
 ; CURRENT FILING DATE: 2003-04-09
 ; PRIOR APPLICATION NUMBER: US 60/328,523
 ; PRIOR FILING DATE: 2001-10-10
 ; PRIOR APPLICATION NUMBER: US 60/344,692
 ; PRIOR FILING DATE: 2001-10-19
 ; PRIOR APPLICATION NUMBER: US 60/387,292
 ; PRIOR FILING DATE: 2002-06-07
 ; PRIOR APPLICATION NUMBER: US 60/391,777
 ; PRIOR FILING DATE: 2002-06-25
 ; PRIOR APPLICATION NUMBER: US 60/396,594
 ; PRIOR FILING DATE: 2002-07-17
 ; PRIOR APPLICATION NUMBER: US 60/404,249
 ; PRIOR FILING DATE: 2002-08-16
 ; PRIOR APPLICATION NUMBER: US 60/407,527
 ; PRIOR FILING DATE: 2002-08-28
 ; NUMBER OF SEQ ID NOS: 75
 ; SOFTWARE: PatentIn version 3.2
 ; SEQ ID NO 45
 ; LENGTH: 1203
 ; TYPE: DNA
 ; ORGANISM: Hepatitis B virus
 US-10-410-962-45

Query Match 88.4%; Score 61; DB 17; Length 1203;
 Best Local Similarity 92.8%; Pred. No. 2.5e-13;
 Matches 64; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 ACACTCTCTCTCAAGAACCTTATGTTTCCTCATGTTGCTGTACAAACCTACGGAC 60
 Db 895 ACGATTCCTCTCAAGAACCTTATGTTTCCTCATGTTGCTGTACAAACCTACGGAC 60
 QY 61 AGAAACTGC 69
 Db 955 GGAACCTGC 963

Search completed: July 26, 2004, 18:07:11
Job time : 230 secs

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OM nucleic - nucleic search, using sw model

Run on: July 26, 2004, 16:17:45 ; Search time 1342 Seconds
(without alignments)
1535.388 Million cell updates/sec

Title: US-09-719-533a-1_COPY_527_595

Perfect score: 69

Sequence: 1 ACAACTCTGCTCAGGAC.....AACCTACGACAGAACTGC 69

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-Processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:

1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_hnc:*
9: gb_est1:*
10: gb_est2:*
11: gb_hnc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: em_gss_hum:*
18: em_gss_inv:*
19: em_gss_pln:*
20: em_gss_vrt:*
21: em_gss_fun:*
22: em_gss_mam:*
23: em_gss_mus:*
24: em_gss_pro:*
25: em_gss_rod:*
26: em_gss_pbg:*
27: em_gss_vrl:*
28: gb_gss1:*
29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
1	28.2	40.9	381	12	EG893479 Kt14h04.Y
2	28	40.6	689	29	CE605031 tigr-gss-
3	27.8	40.3	1068	28	CC184649
4	27.6	40.0	1153	28	CC221988

TITLE
JOURNAL
COMMENT

EG893479 Kt14h04.Y
Contact: McCarter JP
The Washington Univ. Nematode EST Project, 1999
Washington University School of Medicine

Unpublished (1999)

The Washington Univ. Nematode EST Project, 1999

Contact: McCarter JP

The Washington Univ. Nematode EST Project, 1999

Washington University School of Medicine

C	5	27.6	40.0	1254	28	CC286213	CH261-291
C	6	27.4	39.7	792	28	BZ099079	IK155904.
C	7	27.2	39.4	415	13	BY615763	BY615763
C	8	27	39.1	693	29	CC875918	ZMMBB019
C	9	27	39.1	840	28	BZ965578	PUGCM72TD
C	10	26.8	38.8	745	28	AQ752847	HS-5570.B
C	11	26.8	38.8	785	29	CG901218	ZMMBB0050
C	12	26.8	38.8	1021	29	CG398694	ZMMBB001
C	13	26.6	38.6	259	12	BI073599	Kt3212.Y
C	14	26.6	38.6	294	13	BQ091116	Ku1303.Y
C	15	26.6	38.6	294	13	BQ091371	Ku16e05.Y
C	16	26.6	38.6	365	12	BI073816	Kt35404.Y
C	17	26.6	38.6	395	12	BI741821	Kt81611.Y
C	18	26.6	38.6	399	12	BI323723	Kt66003.Y
C	19	26.6	38.6	444	12	BI502157	Kt86a10.Y
C	20	26.6	38.6	447	12	BI450725	Kt73110.Y
C	21	26.6	38.6	458	12	BI323150	Kt62806.Y
C	22	26.6	38.6	459	12	BI323383	Kt70e06.Y
C	23	26.6	38.6	460	12	EG893894	Kt21a06.Y
C	24	26.6	38.6	469	12	BI073332	Kt29f06.Y
C	25	26.6	38.6	470	12	BI323090	Kt61c07.Y
C	26	26.6	38.6	475	12	BI074032	Kt39b08.Y
C	27	26.6	38.6	476	12	BI142702	Kt44906.Y
C	28	26.6	38.6	480	12	BI073334	Kt29f08.Y
C	29	26.6	38.6	492	12	BI073324	Kt29a10.Y
C	30	26.6	38.6	495	12	BI397121	Kt60f03.Y
C	31	26.6	38.6	498	12	BI073466	Kt31b11.Y
C	32	26.6	38.6	556	13	BQ091253	Ku14h09.Y
C	33	26.4	38.3	693	23	CE827261	tigr-gss-
C	34	26.4	38.3	716	28	BH956839	cdn39a07.
C	35	26.4	38.3	916	29	SSC514770	AJ514770 Sus scrof
C	36	26.2	38.0	601	10	BB637242	BB637242
C	37	26.2	38.0	648	13	BY730882	BY730882
C	38	26.2	38.0	655	29	AG147521	Pan trogl
C	39	26.2	38.0	666	29	CG116230	PUDJ011TD
C	40	26.2	38.0	710	13	EX623824	EX623824
C	41	26.2	38.0	747	12	EG648324	EST509943
C	42	26.2	38.0	757	29	CG999075	ZMMBB052
C	43	26.2	38.0	951	29	CG357546	CGMKY51TV
C	44	26.2	38.0	1029	13	BQ058019	AGENCOURT
C	45	26	37.7	514	28	AZ772912	IM0584H09

ALIGNMENTS

EG893479 381 bp mRNA linear EST 04-JUN-2001
Kt14h04.Y1 Strongyloides ratti L1 dAMP v3 Chiapelli McCarter
Strongyloides ratti cDNA 5' similar to TR-Q17459 Q17459 SIMILARITY
TO A PART OF THE TRIPLE-HELICAL REGION OF COLLAGEN ALPHA CHAIN. [1]
;contains element MSRI repetitive element ;, mRNA sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE

EG893479
EG893479.1 GI:14288089

ORGANISM

Strongyloides ratti

Strongyloides ratti

Strongyloides ratti

Strongyloides ratti

Strongyloides ratti

Strongyloides ratti

Strongyloides ratti

Strongyloides ratti

Strongyloides ratti

Strongyloides ratti

Strongyloides ratti

Strongyloides ratti

Strongyloides ratti

Strongyloides ratti

Strongyloides ratti

Strongyloides ratti

Strongyloides ratti

Strongyloides ratti

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: est@watson.wustl.edu
 The library was constructed by Brandi Chiapelli and Dr. James
 McCarter (bchiapell@watson.wustl.edu & jmcarter@watson.wustl.edu) at
 Washington University, St. Louis. DNA Sequencing by: Washington
 University Genome Sequencing Center St. Louis.
 High quality sequence stop: 379.

FEATURES

Location/Qualifiers
 1..381
 /organism="Strongyloides ratti"
 /mol_type="mRNA"
 /db_xref="taxon:34506"
 /dev_stage="L1"
 /lab_host="DH10B"
 /clone_lib="Strongyloides ratti L1 pAMP1 v3 Chiapelli
 McCarter"
 /note="Vector: pAMP1 (Gibco); The library was constructed
 by Brandi Chiapelli and Dr. James McCarter at Washington
 University, St. Louis. The cDNA was made by using
 Dynabead oligo-dT priming (Dyna), PCR based library
 using a modified protocol from the SMART PCR cDNA
 Synthesis Kit from Clontech. Directionally cloned into the
 UDG sites of pAMP1. Nematodes were provided by Dr. Mark
 Viney of Bristol, UK."

ORIGIN

Query Match 40.9%; Score 28.2; DB 12; Length 381;
 Best Local Similarity 68.4%; Pred. No. 25;
 Matches 39; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

QY 12 TCAGGACCTCTATGTTTCCTCATGTTGCTGACAAAACCTACGACGAACTG 68
 |||||
 DB 76 TCAATGAACCTCGTGATTTCTGATGCTGACAACTCTCCGCTGAACTG 132
 |||||

RESULT 2

CE605031
 LOCUS tigr-gss-dog-17000327546513 Dog Library Canis familiaris genomic,
 DEFINITION genomic survey sequence.
 ACCESSION CE605031
 VERSION 22875432
 KEYWORDS GSS.
 SOURCE Canis familiaris (dog)
 ORGANISM Canis familiaris

REFERENCE 1 (bases 1 to 689)
 Kirchner, E.F., Bafna, V., Halpern, A.L., Levy, S., Remington, K.,
 Rusch, D.B., Deicher, A.L., Pop, M., Wang, W., Fraser, C.M. and
 Venter, J.C.
 The dog genome: survey sequencing and comparative analysis
 Science 301 (5641), 1898-1903 (2003)
 MEDLINE 22875432
 PUBMED 14512627
 COMMENT Contact: Kirchner EF
 The Institute for Genomic Research
 Department of Eukaryotic Genomics, TIGR, 9712 Medical Center Drive,
 Rockville, MD 20850, USA
 Tel: 301-838-0200
 Fax: 301-838-0208
 Email: ekirchner@tigr.org
 Class: shotgun.

FEATURES

Location/Qualifiers
 1..689
 /organism="Canis familiaris"
 /mol_type="genomic DNA"
 /strain="Standard Poodle"
 /db_xref="taxon:9615"
 /clone_lib="Dog Library"
 /note="Site_1: BstXI; Libraries were prepared from

ORIGIN

Query Match 40.6%; Score 28; DB 29; Length 689;
 Best Local Similarity 66.7%; Pred. No. 36;
 Matches 40; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

QY 6 TCCTGCTCAGGAACCTCTATGTTTCCTCATGTTGCTGACAAAACCTACGACGAA 65
 |||||
 DB 422 TCCTGCTCAGTCTACTCTCTCTTCTCCATGCTCTCAAAAAAAGAAAGAA 481
 |||||

RESULT 3

CC184649
 LOCUS CC184649/c 1068 bp DNA linear GSS 08-MAY-2003
 DEFINITION CH261-10A21_RM1.1 CH261 Gallus gallus genomic clone CH261-10A21,
 genomic survey sequence.
 ACCESSION CC184649
 VERSION CC184649.1 GI:30428549
 KEYWORDS GSS.
 SOURCE Gallus gallus (chicken)
 ORGANISM Gallus gallus

REFERENCE 1 (bases 1 to 1068)
 Warren, W., Graves, T., Mardis, E. and Wilson, R.
 Gallus gallus BAC End Reads
 Unpublished (2003)
 COMMENT Contact: Richard K. Wilson
 Genome Sequencing Center
 Washington University School of Medicine
 Email: submissions@watson.wustl.edu
 Insert Length: 182000 Std Error: 0.00
 Seq primer: RM1 TACGACTCACTATAGGAGGA
 Class: BAC ends
 High quality sequence start: 37
 High quality sequence stop: 820.
 Location/Qualifiers
 1..1068
 /organism="Gallus gallus"
 /mol_type="genomic DNA"
 /strain="Red Jungle Fowl"
 /db_xref="taxon:9031"
 /clone="CH261-10A21"
 /sex="female"
 /cell_line="UCD001, inbred 256"
 /clone_lib="CH261"
 /note="Vector: pTARBAC2.1; Site 1: EcoRI; Site 2: EcoRI;
 CH261 Female Chicken library - for library and clone
 ordering information: http://www.chori.org/bacpac"

FEATURES

Location/Qualifiers
 1..1068
 /organism="Gallus gallus"
 /mol_type="genomic DNA"
 /strain="Red Jungle Fowl"
 /db_xref="taxon:9031"
 /clone="CH261-10A21"
 /sex="female"
 /cell_line="UCD001, inbred 256"
 /clone_lib="CH261"
 /note="Vector: pTARBAC2.1; Site 1: EcoRI; Site 2: EcoRI;
 CH261 Female Chicken library - for library and clone
 ordering information: http://www.chori.org/bacpac"

FEATURES

Location/Qualifiers
 1..1068
 /organism="Gallus gallus"
 /mol_type="genomic DNA"
 /strain="Red Jungle Fowl"
 /db_xref="taxon:9031"
 /clone="CH261-10A21"
 /sex="female"
 /cell_line="UCD001, inbred 256"
 /clone_lib="CH261"
 /note="Vector: pTARBAC2.1; Site 1: EcoRI; Site 2: EcoRI;
 CH261 Female Chicken library - for library and clone
 ordering information: http://www.chori.org/bacpac"

ORIGIN

Query Match 40.3%; Score 27.8; DB 28; Length 1068;
 Best Local Similarity 74.5%; Pred. No. 49;
 Matches 35; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY 7 CCTGCTCAGGAACCTCTATGTTTCCTCATGTTGCTGACAAAAC 53
 |||||
 DB 966 CATGCCCCAGAAACCTGGTGTTTCCTTAGTTGCCCTCAAAACC 920
 |||||

RESULT 4

CC221988
 LOCUS CC221988 1153 bp DNA linear GSS 12-MAY-2003
 DEFINITION CH261-53N10_Sp6.1 CH261 Gallus gallus genomic clone CH261-53N10,
 genomic survey sequence.
 ACCESSION CC221988
 VERSION CC221988.1 GI:30546761
 KEYWORDS GSS.
 SOURCE Gallus gallus (chicken)
 ORGANISM Gallus gallus

REFERENCE 1 (bases 1 to 1153)
 Warren, W., Graves, T., Mardis, E. and Wilson, R.
 Gallus gallus BAC End Reads
 Unpublished (2003)
 COMMENT Contact: Richard K. Wilson
 Genome Sequencing Center
 Washington University School of Medicine
 Email: submissions@watson.wustl.edu
 Insert Length: 182000 Std Error: 0.00
 Seq primer: RM1 TACGACTCACTATAGGAGGA
 Class: BAC ends
 High quality sequence start: 37
 High quality sequence stop: 820.
 Location/Qualifiers
 1..1153
 /organism="Gallus gallus"
 /mol_type="genomic DNA"
 /strain="Red Jungle Fowl"
 /db_xref="taxon:9031"
 /clone="CH261-53N10"
 /sex="female"
 /cell_line="UCD001, inbred 256"
 /clone_lib="CH261"
 /note="Vector: pTARBAC2.1; Site 1: EcoRI; Site 2: EcoRI;
 CH261 Female Chicken library - for library and clone
 ordering information: http://www.chori.org/bacpac"

RESULT 7
 BY615763/c
 LOCUS
 DEFINITION
 ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM

BY615763 415 bp mRNA linear EST 15-DEC-2002
 BY615763 RIKEN full-length enriched, visual cortex Mus musculus
 cDNA clone K330012B19 3', mRNA sequence.
 BY615763
 EST.
 BY615763.1 GI:26950945
 Mus musculus (house mouse)

Mus musculus
 Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 415)

REFERENCE
 AUTHORS
 CONTACT: Yoshihide Hayashizaki
 Laboratory for Genome Exploration Research Group, RIKEN Genomic
 Sciences Center (GSC), Yokohama Institute
 The Institute of Physical and Chemical Research (RIKEN)
 1-7-22 Suehiro-cho, Teurumi-ku, Yokohama, Kanagawa 230-0045, Japan
 Tel: 81-45-503-9222
 Fax: 81-45-503-9216
 Email: genome-res@gsr.riken.go.jp,
 URL: http://genome.gsc.riken.go.jp/
 Aizawa, K., Akimura, T., Arakawa, T., Carninci, P., Fukuda, S.,
 Hirozane, T., Inotani, K., Ishii, Y., Itoh, M., Kawai, J., Konno, H.,
 Miyazaki, A., Murata, M., Nakamura, M., Nomura, K., Numazaki, R.,
 Ohno, M., Sakai, K., Sakazume, N., Sasaki, D., Sato, K., Shibata, K.,
 Shiraki, T., Tagami, M., Waki, K., Watahiki, A., Muramatsu, M. and
 Hayashizaki, Y. Direct Submission
 Computational Analysis of Full-Length Mouse cDNAs Compared with
 Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
 Normalization and subtraction of cap-trapper-selected cDNAs to
 prepare full-length cDNA libraries for rapid discovery of new
 genes. Genome Res. 10 (10), 1617-1630 (2000)
 RIKEN integrated sequence analysis (RISA) system--384-format
 sequencing pipeline with 384 multicapillary sequencer. Genome Res.
 10 (11), 1757-1771 (2000)
 Computer-based methods for the mouse full-length cDNA
 encyclopedia: real-time sequence clustering for construction of a
 nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
 cDNA library was prepared and sequenced in Mouse Genome

TITLE
 JOURNAL
 MEDLINE
 PUBMED
 COMMENT

Analysis of the mouse transcriptome based on functional annotation
 of 60,770 full-length cDNAs
 Nature 420, 563-573 (2002)
 22354683
 12466851

FEATURES
 source
 Location/Qualifiers
 1..415
 /organism="Mus musculus"
 /mol_type="mRNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="K330012B19"
 /tissue_type="visual cortex"
 /clone_lib="RIKEN full-length enriched, visual cortex"

ORIGIN
 Query Match 39.4%; Score 27.2; DB 13; Length 415;
 Best Local Similarity 64.1%; Pred. No. 60;
 Matches 41; Conservative 0; Mismatches 23; Indels 0; Gaps 0;
 3 AACTCTGCTCAGGAACCTCTATGTTTCCCTCATGTTGCTGTACAAACCTACGACAG 62
 122 AACACGGGCACAGGCAAGTTTACATTTTACACAGATTTCCCTCCACCTACCCACAG 63
 63 AAAC 66
 62 AAAC 59

RESULT 8
 CC875918/c
 LOCUS
 DEFINITION
 ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM

CC875918 693 bp DNA linear GSS 29-JUL-2003
 ZMWBB019N08.f ZMWBBB Zea mays subsp. mays genomic clone
 ZMWBB019N08 5', genomic survey sequence.
 CC875918
 GSS.
 CC875918.1 GI:33305593
 Zea mays subsp. mays (maize)
 Zea mays subsp. mays
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACAD
 clade; Panicoideae; Andropogoneae; Zea.
 Yu, Y., Kim, H.R., Hatfield, J., Soderlund, C., Bharti, A.K., Messing, J.
 and Wing, R.
 Sequencing of the maize genome
 Unpublished (2003)
 Contact: Rod Wing
 Arizona Genomics Institute
 University of Arizona
 Biological Sciences West, 448A, P.O. Box 210088, Tucson, AZ
 85721-0088, USA
 Tel: 520 626 3967
 Fax: 520 621 9288
 Email: http://genome.arizona.edu
 PCR Primers
 FORWARD: T7
 BACKWARD: M13r
 Plate: 0190 row: N column: 08
 Seq primer: T7
 Class: BAC ends.

FEATURES
 source
 Location/Qualifiers
 1..693
 /organism="Zea mays subsp. mays"
 /mol_type="genomic DNA"
 /cultivar="B73"
 /sub_species="mays"
 /db_xref="taxon:4578"

Encyclopedia Project of Genome Exploration Research Group in Riken
 Genomic Sciences Center and Genome Science Laboratory in RIKEN.
 Division of Experimental Animal Research in Riken contributed to
 prepare mouse tissues.
 Tissues were provided by Michela Fagiolini and Takao K. Hensch (
 Laboratory for Neuronal Circuit Development Brain Science Institute
 RIKEN 2-1 Hiroosawa, Wako-shi, Saitama 351-0198 Japan) whose
 assistance we gratefully acknowledge.
 Please visit our web site (<http://genome.gsc.riken.go.jp>) for
 further details.


```

/clone="ZMMBB0190N08"
/lab_host="DH103"
/clone_lib="ZMMBB"
/notes="vector: pBelcBAC11; Site 1: HindIII; Site 2:
HindIII; Zea mays L. ssp. mays"

ORIGIN
Query Match          39.1%; Score 27; DB 29; Length 693;
Best Local Similarity 70.6%; Pred. No. 82;
Matches 36; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

QY 2 CAACCTCTGCTCAGGAACTCTATGTTTCCCTCATGTTCTGTACAAAC 52
Db 680 CAACCTCTGTTGAACAACTCTGCTTCTACCACTTCGGCTCTTAC 630

RESULT 9
BZ965578 840 bp DNA linear GSS 25-MAR-2003
LOCUS PUGGM72TD.ZM.0.6.1.0.KB.Zea mays genomic clone ZMMBTa379K23,
DEFINITION Genomic survey sequence.
ACCESSION BZ965578
VERSION BZ965578.1 GI:29181484
KEYWORDS GSS.
SOURCE Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACAD
clade; Panicoideae; Andropogoneae; Zea.
REFERENCE 1 (bases 1 to 840)
AUTHORS Whitelaw,C.A., Quackenbush,J., Van Aken,S., Utterback,T.,
Reinick,A., Fraser,C.M., Yuan,Y., San Miguel,P., Ma,J. and
Bennetzen,J.
Maize Genomics Consortium
Unpublished (2003)
Other GSSs: PUGGM72TB
Contact: Cathy Whitelaw
TIGR
9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-838-5843
Fax: 301-838-0208
Email: whitelaw@tigr.org
Seq primer: Tg
Class: sheared ends.
FEATURES
Source
1..840
/organism="Zea mays"
/mol_type="genomic DNA"
/strain="B73"
/db_xref="taxon:4577"
/clone="ZMMBTa379K23"
/clone_lib="ZM 0.6 1.0 KB"
/notes="vector: pCR4-TOPO; Site 1: EcoRI; 0.6-1.0 kb high
Cot selected genomic DNA library"

ORIGIN
Query Match          39.1%; Score 27; DB 28; Length 840;
Best Local Similarity 62.7%; Pred. No. 87;
Matches 42; Conservative 0; Mismatches 25; Indels 0; Gaps 0;

QY 1 ACAACTCTGCTCAGGAACTCTATGTTTCCCTCATGTTCTGTACAAACCTACGGAC 60
Db 233 ACAACTGCTGTCAGGCAACTCTATGTTTCCCTCATGTTCTGTATGTGCGCAACCATGGTC 174

QY 61 AGAAACT 67
Db 173 GTTACCT 167

RESULT 10
AQ752847 745 bp DNA linear GSS 19-JUL-1999
LOCUS HS_5570_B1_B01_SP6_RPCI-11 Human Male BAC Library Homo sapiens
DEFINITION
```

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genomic clone Plate=1146 Col=1 Row=D, genomic survey sequence.
ACCESSION AQ752847 GI:5540005
VERSION AQ752847.1
KEYWORDS GSS.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 745)
AUTHORS Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T., and
Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and
Hood,L.
Sequence-tagged connectors: A sequence approach to mapping and
scanning the human genome
Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
JOURNAL 99380589
MEDLINE 10449784
PUBMED
COMMENT Contact: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3618
Fax: (206) 616-3887
Email: jwallace@u.washington.edu
Clones are derived from the human BAC library RPCI-11. For BAC
library availability, please contact Pieter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering_bac.htm)
or from Resear h Genetics (info@resgen.com). BAC end Web Server:
http://www.htsc.washington.edu
Plate: 1146 row: D column: 1
Seq primer: SP6
Class: BAC ends
High quality sequence stop: 745.
FEATURES
Source
1..745
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/clone="Plate=1146 Col=1 Row=D"
/sex="male"
/clone_lib="RPCI-11 Human Male BAC Library"
/notes="vector: pBACe3.6; Site 1: EcoRI; Site 2: EcoRI;
Male blood DNA was isolated from one randomly chosen donor
and partially digested with a combination of EcoRI and
EcoRI Methylase. Size selected DNA was cloned into the
pBACe3.6 vector at EcoRI sites"

ORIGIN
Query Match          38.8%; Score 26.8; DB 28; Length 745;
Best Local Similarity 64.5%; Pred. No. 99;
Matches 40; Conservative 0; Mismatches 22; Indels 0; Gaps 0;

QY 4 ACTCCTGCTCAGGAACTCTATGTTTCCCTCATGTTCTGTACAAACCTACGGACAG 63
Db 7 ACTGCTGGGAACAACTCTCACTCTGCATTTCTCATGTTCTGCACAGAACTTCTGACCAA 66

QY 64 AA 65
Db 67 AA 68

RESULT 11
CG901218 785 bp DNA linear GSS 09-DEC-2003
LOCUS ZMMBB0508G03f.ZMMBBb (HindIII) Zea mays subsp. mays genomic clone
DEFINITION ZMMBBb0508G03 5', genomic survey sequence.
ACCESSION CG901218
VERSION CG901218.1 GI:39600485
KEYWORDS GSS.
SOURCE Zea mays subsp. mays (maize)
ORGANISM Zea mays subsp. mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
```

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.

REFERENCE
1 (bases 1 to 785)

AUTHORS
Bharti, A.K., Young, S., Kavchok, S., Keizer, G., Bronzino, A.C., Zohovetz, V., Fuks, G., Yu, Y., Wing, R. and Messing, J.

TITLE
Sequencing of the maize genome at PGIR (2003c)

JOURNAL
Unpublished (2003)

COMMENT
Contact: Bharti, A.K.
Dr. Joachim Messing's lab
The Plant Genome Initiative at Rutgers, Waksman Institute, Rutgers University
190 Frelinghuysen Road, Piscataway, NJ 08854, USA
Tel: 732 445 3801
Fax: 732 445 5735
Email: bharti@waksman.rutgers.edu
Seq primer: T7
Class: BAC ends
High quality sequence start: 116.

FEATURES
source
Location/Qualifiers
1..785
/organism="Zea mays subsp. mays"
/mol_type="genomic DNA"
/cultivar="B73"
/sub_species="mays"
/db_xref="taxon:4578"
/clone="ZMMBB0508G03"
/lab_host="E. coli DH10B"
/clone_lib="ZMMBBB (HindIII)"
/note="Vector: pCUGI; Site_1: HindIII; Site_2: HindIII"

ORIGIN

Query Match 38.8%; Score 26.8; DB 29; Length 785;
Best Local Similarity 64.5%; Pred. No. 1e+02;
Matches 40; Conservative 0; Mismatches 22; Indels 0; Gaps 0;

QY 3 AACTCTGCTCAAGAACCTCTATGTTCCCTCATGTTGCTGACAAAACCTACGACAG 62
|||||
Db 311 AACTCTGCTCAAGAACCTCTATGTTCCCTCATGTTGCTGACAAAACCTACGACAG 62
|||||

QY 63 AA 64
||
Db 371 AA 372

RESULT 12
CG398694

LOCUS
CG398694 1021 bp DNA linear GSS 22-SEP-2003
ZMMBB0019E20f ZMMBBc (EcoRI) Zea mays subsp. mays genomic clone

DEFINITION
CG398694

ACCESSION
CG398694

VERSION
GSS.

KEYWORDS
Zea mays subsp. mays (maize)

SOURCE
Zea mays subsp. mays

ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.

REFERENCE
1 (bases 1 to 1021)

AUTHORS
Bharti, A.K., Young, S., Kavchok, S., Keizer, G., Bronzino, A.C., Rouzard, K., Fuks, G., Yu, Y., Wing, R. and Messing, J.

TITLE
Sequencing of the maize genome at PGIR (2003b)

JOURNAL
Unpublished (2003)

COMMENT
Contact: Bharti, A.K.
Dr. Joachim Messing's lab
The Plant Genome Initiative at Rutgers, Waksman Institute, Rutgers University
190 Frelinghuysen Road, Piscataway, NJ 08854, USA
Tel: 732 445 3801
Fax: 732 445 5735
Email: bharti@waksman.rutgers.edu
Seq primer: T7
Class: BAC ends
High quality sequence start: 57.

FEATURES
source
Location/Qualifiers
1..1021
/organism="Zea mays subsp. mays"
/mol_type="genomic DNA"
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Matches 40; Conservative 0; Mismatches 22; Indels 0; Gaps 0;

QY 3 AACTCTGCTCAAGAACCTCTATGTTCCCTCATGTTGCTGACAAAACCTACGACAG 62
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Db 306 AACTCTGCTCAAGAACCTCTATGTTCCCTCATGTTGCTGACAAAACCTACGACAG 62
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QY 63 AA 64
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Db 366 AA 367

RESULT 13
BI073599

LOCUS
BI073599 259 bp mRNA linear EST 19-JUN-2001
kt32f12.y1 Strongyloides ratti L2 pAMP1 v1 Chiapelli McCarter

DEFINITION
Strongyloides ratti cDNA 5' similar to TR:Q19528 Q19528 F1C8.2
PROTEIN: [1] ; contains element PTR7 repetitive element 1, mRNA sequence.

ACCESSION
BI073599

VERSION
BI073599.1 GI:14494219

KEYWORDS
EST.

SOURCE
Strongyloides ratti

ORGANISM
Strongyloides ratti

REFERENCE
1 (bases 1 to 259)

AUTHORS
McCart, J., Clifton, S., Chiapelli, B., Pape, D., Martin, J., Wylie, T., Dante, M., Marra, M., Hillier, L., Kucaba, T., Theising, B., Bowers, Y., Gibbons, M., Ritter, E., Bennett, J., Franklin, C., Tsagaris, V., Ronko, I., Kennedy, S., Maguire, L., Beck, C., Harwood, K., Steptoe, M., Allen, M., Person, B., Swaller, I., Harvey, N., Schurk, R., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R. and Wilson, R.

TITLE
The Washington Univ. Nematode EST Project, 1999

JOURNAL
Unpublished (1999)

COMMENT
Contact: McCarter JP
The Washington Univ. Nematode EST Project, 1999
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@wustl.edu
The library was constructed by Brandi Chiapelli and Dr. James McCarter (bchiapell@wustl.edu & jmcarter@wustl.edu) at Washington University, St. Louis. DNA Sequencing by: Washington University Genome Sequencing Center St. Louis.
Seq primer: -40RP from Gibco
High quality sequence stop: 191.

FEATURES
source
Location/Qualifiers
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/note="Vector: pAMP1 (Gibco); The library was constructed

by Brandi Chiapelli and Dr. James McCarter at Washington University, St. Louis. The cDNA was made by using Dynabead oligo-dt priming (Dyna). PCR based library using a modified protocol from the SMART PCR cDNA Synthesis kit from Clontech. Directionally cloned into the UDG sites of pAMP1. Nematodes were provided by Dr. Mark Viney of Bristol, UK.

ORIGIN

Query Match 38.6%; Score 26.6; DB 12; Length 259;
Best Local Similarity 66.7%; Pred. No. 84;
Matches 38; Conservative 0; Mismatches 19; Indels 0; Gaps 0;
QY 12 TCAAGGAACCTCTATGTTCCCTCATGTTGCTGTACAAAACCTACGACAGAACTG 68
Db 81 TCAATGAACCTCGTATTCGTTCTCATGTTGCTGTACAAAATTTCCGTCGAACTG 137

RESULT 14
LOCUS BQ091116 294 bp mRNA linear EST 05-APR-2002
DEFINITION ku13b03.v1 Strongyloides ratti L2 pAMP1 v1 Chiapelli McCarter
Strongyloides ratti cDNA 5' similar to TR:Q17418 Q17418 B0024.2
PROTEIN. [1] ; contains element MSR1 repetitive element ;, mRNA
sequence.
ACCESSION BQ091116
VERSION BQ091116.1 GI:20065317
KEYWORDS EST.
SOURCE Strongyloides ratti
ORGANISM Strongyloides ratti
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;
Panagrolaimidae; Strongyloidea; Strongyloides.
REFERENCE 1 (bases 1 to 294)
AUTHORS McCarter,J., Clifton,S., Chiapelli,B., Pape,D., Martin,J.,
Wyllie,T., Dante,M., Marra,M., Hillier,L., Kucaba,T., Theising,B.,
Bowers,Y., Gibbons,M., Rutter,E., Bennett,J., Franklin,C.,
Tsagarisshvili,R., Ronko,I., Kennedy,S., Maguire,L., Beck,C.,
Underwood,K., Steptoe,M., Allen,M., Person,B., Swaller,T.,
Harvey,N., Schurk,R., Kohn,S., Shin,T., Jackson,Y., Cardenas,M.,
McCann,R., Waterston,R. and Wilson,R.
The Washington Univ. Nematode EST Project, 1999
Unpublished (1999)
CONTACT: McCarter JP

TITLE The Washington Univ. Nematode EST Project, 1999
JOURNAL
COMMENT The Washington Univ. Nematode EST Project, 1999
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
The library was constructed by Brandi Chiapelli and Dr. James
McCarter (bchiapel@watson.wustl.edu & jmccarte@watson.wustl.edu) at
Washington University, St. Louis. DNA Sequencing by: Washington
University Genome Sequencing Center St. Louis.
Location/Qualifiers
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/clone_lib="Strongyloides ratti L2 pAMP1 v1 Chiapelli
McCarter"

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/organism="Strongyloides ratti"
/mol_type="mRNA"
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McCarter"
/note="Vector: pAMP1 (Gibco); The library was constructed
by Brandi Chiapelli and Dr. James McCarter at Washington
University, St. Louis. The cDNA was made by using
Dynabead oligo-dt priming (Dyna). PCR based library
using a modified protocol from the SMART PCR cDNA
Synthesis kit from Clontech. Directionally cloned into the
UDG sites of pAMP1. Nematodes were provided by Dr. Mark
Viney of Bristol, UK."

ORIGIN

Query Match 38.6%; Score 26.6; DB 13; Length 294;
Best Local Similarity 66.7%; Pred. No. 88;
Matches 38; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

Best Local Similarity 66.7%; Pred. No. 88;
Matches 38; Conservative 0; Mismatches 19; Indels 0; Gaps 0;
QY 12 TCAAGGAACCTCTATGTTCCCTCATGTTGCTGTACAAAACCTACGACAGAACTG 68
Db 110 TCAATGAACCTCGTATTCGTTCTCATGTTGCTGTACAAAATTTCCGTCGAACTG 166

ORIGIN

RESULT 15
LOCUS BQ091371 294 bp mRNA linear EST 05-APR-2002
DEFINITION ku16e05.v1 Strongyloides ratti L2 pAMP1 v1 Chiapelli McCarter
Strongyloides ratti cDNA 5' similar to TR:Q17418 Q17418 B0024.2
PROTEIN. [1] ; contains element MSR1 repetitive element ;, mRNA
sequence.
ACCESSION BQ091371
VERSION BQ091371.1 GI:20065572
KEYWORDS EST.
SOURCE Strongyloides ratti
ORGANISM Strongyloides ratti
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;
Panagrolaimidae; Strongyloidea; Strongyloides.
REFERENCE 1 (bases 1 to 294)
AUTHORS McCarter,J., Clifton,S., Chiapelli,B., Pape,D., Martin,J.,
Wyllie,T., Dante,M., Marra,M., Hillier,L., Kucaba,T., Theising,B.,
Bowers,Y., Gibbons,M., Rutter,E., Bennett,J., Franklin,C.,
Tsagarisshvili,R., Ronko,I., Kennedy,S., Maguire,L., Beck,C.,
Underwood,K., Steptoe,M., Allen,M., Person,B., Swaller,T.,
Harvey,N., Schurk,R., Kohn,S., Shin,T., Jackson,Y., Cardenas,M.,
McCann,R., Waterston,R. and Wilson,R.
The Washington Univ. Nematode EST Project, 1999
Unpublished (1999)
CONTACT: McCarter JP

TITLE The Washington Univ. Nematode EST Project, 1999
JOURNAL
COMMENT The Washington Univ. Nematode EST Project, 1999
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
The library was constructed by Brandi Chiapelli and Dr. James
McCarter (bchiapel@watson.wustl.edu & jmccarte@watson.wustl.edu) at
Washington University, St. Louis. DNA Sequencing by: Washington
University Genome Sequencing Center St. Louis.
Location/Qualifiers
1. .294
/organism="Strongyloides ratti"
/mol_type="mRNA"
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McCarter"

ORIGIN

Query Match 38.6%; Score 26.6; DB 13; Length 294;
Best Local Similarity 66.7%; Pred. No. 88;
Matches 38; Conservative 0; Mismatches 19; Indels 0; Gaps 0;
QY 12 TCAAGGAACCTCTATGTTCCCTCATGTTGCTGTACAAAACCTACGACAGAACTG 68
Db 110 TCAATGAACCTCGTATTCGTTCTCATGTTGCTGTACAAAATTTCCGTCGAACTG 166

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Job time : 1346 secs

Wed Jul 28 14:34:15 2004

us-09-719-533a-1_copy_527_595.rst

Page 8

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: July 26, 2004, 12:21:09 ; Search time 3003 Seconds
(without alignments)
9829.040 Million cell updates/sec

Title: US-09-719-533A-1_COPY_155_835

Perfect score: 681

Sequence: 1 ATGAGACATCCGATCAGG.....GTCTTTGGGTATACATTAA 681

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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1: gb_ba:*

2: gb_htg:*

3: gb_in:*

4: gb_om:*

5: gb_ov:*

6: gb_pat:*

7: gb_ph:*

8: gb_pl:*

9: gb_pr:*

10: gb_ro:*

11: gb_sts:*

12: gb_sy:*

13: gb_un:*

14: gb_vi:*

15: em_ba:*

16: em_fun:*

17: em_hum:*

18: em_in:*

19: em_mu:*

20: em_om:*

21: em_or:*

22: em_ov:*

23: em_pat:*

24: em_ph:*

25: em_pl:*

26: em_ro:*

27: em_sts:*

28: em_un:*

29: em_vi:*

30: em_htg_hum:*

31: em_htg_inv:*

32: em_htg_other:*

33: em_htg_mus:*

34: em_htg_pln:*

35: em_htg_rod:*

36: em_htg_mam:*

37: em_htg_vrt:*

38: em_sy:*

39: em_htgo_hum:*

40: em_htgo_mus:*

41: em_htgo_other:*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	681	100.0	3215	6	BD232230	BD232230 Hepatitis
2	676.2	99.3	3215	14	AB073834	AB073834 Hepatitis
3	676.2	99.3	3215	14	AF100308	AF100308 Hepatitis
4	676.2	99.3	3215	14	AF100309	AF100309 Hepatitis
5	676.2	99.3	3215	14	AF121243	AF121243 Hepatitis
6	676.2	99.3	3215	14	AF121243	AF121243 Hepatitis
7	676.2	99.3	3215	14	AF121246	AF121246 Hepatitis
8	676.2	99.3	3215	14	AF167097	AF167097 Hepatitis
9	674.6	99.1	3215	14	AB073822	AB073822 Hepatitis
10	674.6	99.1	3215	14	AB073827	AB073827 Hepatitis
11	674.6	99.1	3215	14	AB073828	AB073828 Hepatitis
12	674.6	99.1	3215	14	AF121244	AF121244 Hepatitis
13	674.6	99.1	3215	14	AF121249	AF121249 Hepatitis
14	674.6	99.1	3215	14	AF282918	AF282918 Hepatitis
15	674.6	99.1	3215	14	AF479684	AF479684 Hepatitis
16	674.6	99.1	3215	14	HEVP6CSX	X97851 Hepatitis B
17	673.8	98.9	3215	14	AB073840	AB073840 Hepatitis
18	673	98.8	1431	14	AF291830	AF291830 Hepatitis
19	673	98.8	1758	14	AF279464	AF279464 Hepatitis
20	673	98.8	3215	14	AB073826	AB073826 Hepatitis
21	673	98.8	3215	14	AF167089	AF167089 Hepatitis
22	673	98.8	3215	14	AY220703	AY220703 Hepatitis
23	673	98.8	3215	14	HPBADW2	D00330 Hepatitis B
24	672.2	98.7	3215	14	AB073821	AB073821 Hepatitis
25	671.4	98.6	681	14	AF061527	AF061527 Hepatitis
26	671.4	98.6	681	14	AF397207	AF397207 Hepatitis
27	671.4	98.6	1381	14	S74815	SV4815 pre-S regio
28	671.4	98.6	3213	14	AY217369	AY217369 Hepatitis
29	671.4	98.6	3215	14	AB073837	AB073837 Hepatitis
30	671.4	98.6	3215	14	AY217356	AY217356 Hepatitis
31	671.4	98.6	3215	14	AY217362	AY217362 Hepatitis
32	671.4	98.6	3248	14	AY206377	AY206377 Hepatitis
33	671	98.5	3215	14	AB073831	AB073831 Hepatitis
34	671	98.5	3215	14	AF167094	AF167094 Hepatitis
35	670.2	98.4	3215	14	AF121247	AF121247 Hepatitis
36	669.8	98.4	681	6	AR026126	AR026126 Sequence
37	669.8	98.4	681	6	AR026128	AR026128 Sequence
38	669.8	98.4	3212	14	AY217365	AY217365 Hepatitis
39	669.8	98.4	3214	14	HBV131133	AJ131133 Hepatitis
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42	669.8	98.4	3215	14	AF167093	AF167093 Hepatitis
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ALIGNMENTS

RESULT 1

BD232230

LOCUS

DEFINITION

Hepatitis B virus strains appearing by vaccine administration and

utilization thereof.

ACCESSION

BD232230

VERSION

BD232230.1 GI:33042000

KEYWORDS

JP 2002518013-A/1.

SOURCE

unidentified

ORGANISM

unclassified.

REFERENCE

1 (bases 1 to 3215)

AUTHORS

Oon,C.J., Lim,G.K., Leong,A.L., Zhao,Y. and Chen,W.N.

TITLE

Hepatitis B virus strains appearing by vaccine administration and

utilization thereof

BD232230 3215 bp DNA linear PAT 17-JUL-2003
Hepatitis B virus strains appearing by vaccine administration and
utilization thereof.

JOURNAL
Patent: JP 2002518013-A 1 25-JUN-2002;
GOVERNMENT OF THE REPUBLIC OF SINGAPORE
COMMENT
OS Unidentified
PN JP 2002518013-A/1
PD 25-JUN-2002
PF 19-JUN-1998 JP 2000554856
PI CHONG JIN OON, GEK KEOW LIM, AI LIN LEONG, YI ZHAO, WEI NING CHEN
PC C12N15/09, A61K39/29, A61K45/00, A61P1/16, A61P31/20, A61P35/00, PC
C07K14/02,
C07K16/08, C12N7/00, C12P21/02, C12P21/08, C12Q1/68, G01N33/53, PC
G01N33/53,
PC G01N33/566, G01N33/576, C12N15/00
CC Strandedness: Double;
CC Topology: Circular;
CC Hepatitis B virus strains appearing by vaccine administration
CC and
CC utilization thereof
FH Key Location/Qualifiers
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FT
FT
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Db 155 ATGGAGACATCGATCAGGACTCCTAGGACCCCTGCTCGTGTACAGGGGGTTTTC 214
Qy 61 TTGTTGACAAAATCCTCACAATACCGCAGAGTCTAGACTCGTGGTGCATTTCTCAAT 120
Db 215 TTGTTGACAAAATCCTCACAATACCGCAGAGTCTAGACTCGTGGTGCATTTCTCAAT 274
Qy 121 TTCTAGGGGAACACCGGTGTCTTGGCCAAAATTCGCAGTCCCAAAATCTCCAGTCAC 180
Db 275 TTCTAGGGGAACACCGGTGTCTTGGCCAAAATTCGCAGTCCCAAAATCTCCAGTCAC 334
Qy 181 TCACCAACTGTGTCTCCTCAATTTGCTGATGCTGGATGTCTGCGCGGTTTT 240
Db 335 TCACCAACTGTGTCTCCTCAATTTGCTGATGCTGGATGTCTGCGCGGTTTT 394
Qy 241 ATCATCTTCTCTGATCCTGCTGATGCTGATCTCTTGTGTTCTTCTGGACTAT 300
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Qy 361 TCGAAAACCTGCAAACTCTGCTCAAGAACTCTATGTTTCCCTCATGTTGCTGAC 420
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Db 815 TGTCTTTGGTATACATTTAA 835
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DEFINITION AB073834
ACCESSION AB073834
VERSION AB073834.1 GI:21280253
KEYWORDS
SOURCE Hepatitis B virus
ORGANISM Hepatitis B virus
VIRUSES; Retroviral viruses; Hepadnaviridae; Orthohepadnavirus.
REFERENCE
1 Sugauchi, F., Orito, E., Ichida, T., Kato, H., Sakugawa, H., Kakumu, S.,
Ishida, T., Chutaputti, A., Lai, C.L., Ueda, R., Miyakawa, Y. and
Mizokami, M.
Hepatitis B virus of genotype B with or without recombination with
genotype C over the precore region plus the core gene
J. Virol. 76 (12), 5985-5992 (2002)
22016130
PUBMED 12021331
REFERENCE 2 (bases 1 to 3215)
AUTHORS Sugauchi, F., Orito, E., Kato, H., Ueda, R. and Mizokami, M.
TITLE Direct Submission
JOURNAL Submitted (01-NOV-2001) Fuminaka Sugauchi, Nagoya City University
MEDLINE Medical School Graduate School of Science, Department of Internal
Medicine and Molecular Science; Mizuho, Nagoya, Aichi 467-8601,
Japan [E-mail: suga@med.nagoya-cu.ac.jp, Tel:81-52-853-8216,
Fax:81-52-842-0021]
FEATURES
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Best Local Similarity 99.6%; Pred. No. 2.4e-187;
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Qy 181 TCACCAACTGTGTCTCCTCAATTTGCTGATGCTGGATGTCTGCGCGGTTTT 240
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Qy 541 CAGTGGTCTGAGGCTTTCCCGCACTGCTGGCTTTTCAGTTATATGATGATGTGTTT 600
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Db 335 TCACCAACCTGTTGCTCTCCCAATTTGCTCGTGGTTATCGCTGGATGTGTCTGGCGGCTTTT 394
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Qy 301 CAAGGTATGTTGCGCGTTTCTGCTCTAAATCCAGGATCAACAACCAACCGACCGACCA 360
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Qy 361 TGAACCACTGCAACATCTGCTCAAGAACCTCTATGTTTCCCTCATGTTGCTGTACA 420
Db 515 TGAACCACTGCAACATCTGCTCAAGAACCTCTATGTTTCCCTCATGTTGCTGTACA 574
Qy 421 AAACCTACGACAGAAATCTGCTATATCCCATCCATCCATCTTGGGCTTTCCGAAAA 480
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RESULT 3
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LOCUS Hepatitis B virus strain 2-18, complete genome.
DEFINITION
ACCESSION AF100308
VERSION
KEYWORDS
SOURCE
ORGANISM
Hepatitis B virus
Hepatitis B virus
Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
REFERENCE
1 (sites)
Wen, Y.
Sequence and functional study on hepatitis B virus in pregnant
women in association with failure of protection by postexposure
immunization in infants
Unpublished
2 (bases 1 to 3215)
Wen, Y.
Direct Submission
Submitted (15-OCT-1998) Department of Molecular Virology, Shanghai
Medical University, 138 Yi Xue Yuan Road, Shanghai 20032, China
Location/Qualifiers

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ORIGIN

Query Match 99.3%; Score 676.2; DB 14; Length 3215;
Best Local Similarity 99.6%; Pred. No. 2.4e-187;
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RESULT 5
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DEFINITION Hepatitis B virus isolate HBV/14611, complete genome.
ACCESSION AF121243
VERSION AF121243.1 GI:6692482
KEYWORDS
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ORGANISM
REFERENCE
AUTHORS Hannoun, C., Hoxal, P. and Lindh, M.
TITLE Long-term mutation rates in the hepatitis B virus genome
JOURNAL J. Gen. Virol. 81 (Pt 1), 75-83 (2000)
MEDLINE 20109034
PUBMED 10640544
REFERENCE 2 (bases 1 to 3215)
AUTHORS Hannoun, C., Hoxal, P. and Lindh, M.
TITLE Direct Submission
JOURNAL Submitted (19-JAN-1999) Clinical Virology, Laboratory Medicine,
Guldhedssatan 10B, Goteborg 413 46, Sweden
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ORIGIN		Query Match	99.3%;	Score 676.2;	DB 14;	Length 3215;
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		Matches 678;	Conservative 0;	Mismatches 3;	Indels 0;	Gaps 0;
QY	1	ATGGAGAAATCGCATCAGGACTCCTAGGACCCCTGCTGCTGTATCAGCGGGGTTTTTC	60			
Db	155	ATGGAGAAATCGCATCAGGACTCCTAGGACCCCTGCTGCTGTATCAGCGGGGTTTTTC	214			
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Db	215	TTGTGTGACAAAATCCCTCACAAATCCGACAGAGCTAGACTCGGTGGGACTTCTCTCAAT	274			
QY	121	TTTCTAGGGGGAACACCGGTGTGCTTGTGGCCAAAATTGCGAGTCCCAATCTCCAGTCAC	180			
Db	275	TTTCTAGGGGGAACACCGGTGTGCTTGTGGCCAAAATTGCGAGTCCCAATCTCCAGTCAC	334			
QY	181	TCACCAACCTGTTGTTCCTCCAAATTGTCCCTGGTTATCGCTGGAGTGTCTGTGGGGGTTTT	240			
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ORIGIN

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				0;	Gaps
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DB	155	ATGGAGAACATCGCATCAGGACTCCTAGGACCCCTGCTCGTGTTCACAGCGGGGTTTTC	214		
QY	61	TTGTTTGACAAAAATCCTCACAAATACCGCAGAGTCTAGACTCGTGGTGACCTTCTCTCAAT	120		
DB	215	TTGTTTGACAAAAATCCTCACAAATACCGCAGAGTCTAGACTCGTGGTGACCTTCTCTCAAT	274		
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QY	181	TCACCAACCTGTGTCCTCCAAATTTGCTGGTTATCGCTGGATGTGTCTGCGCGGTTT	240		
DB	335	TCACCAACCTGTGTCCTCCAAATTTGCTGGTTATCGCTGGATGTGTCTGCGCGGTTT	394		
QY	241	ATCATCTTCTCTGCTGCTGCTATCGCTCATCTTCTTGTGGTCTTCTTGGACTAT	300		
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DB	815	TGCTTTTGGGTATACATTTAA	835		

RESULT 8

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DEFINITION Hepatitis B virus isolate Iiib, complete genome.
ACCESSION AY167097
VERSION AY167097.1 GI:32346284
KEYWORDS

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SOURCE Hepatitis B virus
ORGANISM Viruses; Retroviridae; Hepadnaviridae; Orthohepadnavirus.

REFERENCE 1 (bases 1 to 3215)
AUTHORS Liu, C.-J., Chen, P.-J., Lai, M.-Y., Kao, J.-H. and Chen, D.-S.
TITLE A prospective study characterizing full-length hepatitis B virus genomes during acute exacerbation
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 3215)
AUTHORS Liu, C.-J., Chen, P.-J., Lai, M.-Y., Kao, J.-H. and Chen, D.-S.
TITLE Direct Submission
JOURNAL Submitted (21-OCT-2002) Hepatitis Research Center, National Taiwan University Hospital, 1 Chang-Te Street, Taipei 100, Taiwan

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Best Local Similarity 99.6%; Pred. No. 2.4e-187;
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DEFINITION Hepatitis B virus DNA, complete genome, isolate:HBV-Chi32.
ACCESSION AB073822
VERSION AB073822.1 GI:21280229
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REFERENCE 1 Sugauchi, F., Orito, E., Ichida, T., Kato, H., Sakugawa, H., Kakumu, S.,
Ishida, T., Chutaputti, A., Lai, C.L., Ueda, R., Miyakawa, Y. and
Mizokami, M.
Hepatitis B virus of genotype B with or without recombination with
genotype C over the precore region plus the core gene
J. Virol. 76 (12), 5985-5992 (2002)
22016130
PUBMED 12021331
REFERENCE 2 (bases 1 to 3215)
AUTHORS Sugauchi, F., Orito, E., Kato, H., Ueda, R. and Mizokami, M.
TITLE Direct Submission
JOURNAL Submitted (01-NOV-2001) Fuminaka Sugauchi, Nagoya City University
TITLE Medical School Graduate School of Science, Department of Internal
JOURNAL Medicine and Molecular Science, Mizuho, Nagoya, Aichi 467-8601,
Japan [E-mail:suga@med.nagoya-cu.ac.jp, Tel:81-52-853-8216,
Fax:81-52-842-0021]

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AB073828      VERSION
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Hepatitis B virus
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Sugauchi,F., Orito,E., Ichida,T., Kato,H., Sakugawa,H., Kakumu,S.,
Ishida,T., Chutaputti,A., Lai,C.L., Ueda,R., Miyakawa,Y. and
Mizokami,M.
Hepatitis B virus of genotype B with or without recombination with
genotype C over the precore region plus the core gene
J. Virol. 76 (12), 5985-5992 (2002)
22016130
12021331
2 (bases 1 to 3215)
Sugauchi,F., Orito,E., Kato,H., Ueda,R. and Mizokami,M.
Direct Submission
Submitted (01-NOV-2001) Fuminaka Sugauchi, Nagoya City University
Medical School Graduate School of Science, Department of Internal
Medicine and Molecular Science; Mizuho, Nagoya, Aichi 467-8601,
Japan [E-mail:sugamed.nagoya-cu.ac.jp, Tel:81-52-853-8216,
Fax:81-52-842-0021]
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SOURCE

gene

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REFERENCE 2 (bases 1 to 3215)
AUTHORS Hamoun, C., Horal, P. and Lindh, M.
TITLE Direct Submission
JOURNAL Submitted (19-JAN-1999) Clinical Virology, Laboratory Medicine,
Guilhedsgatan 10B, Goteborg 413 46, Sweden
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Best Local Similarity 99.4%; Pred. No. 7.2e-187;
Matches 677; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
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DB 155 ATGAGAACATCGCATCAGGACTCCTAGGACCCCTGCTGTTTACAGGCGGGTTTTTC 214
QY 61 TTGTTGACAAAAATCCTCAAAATACCCAGAGTCTAGACTCGTGGTGACTTCTCTCAAT 120
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ACCESSION AF121249
VERSION AF121249.1 GI:6692488
KEYWORDS
SOURCE
ORGANISM
Hepatitis B virus
Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
REFERENCE
AUTHORS Hannoun,C., Horal,P. and Lindh,M.
TITLE Long-term mutation rates in the hepatitis B virus genome
JOURNAL J. Gen. Virol. 81 (Pt 1), 75-83 (2000)
MEDLINE 20109034
PUBMED 10640544
REFERENCE
AUTHORS Hannoun,C., Horal,P. and Lindh,M.
TITLE Direct Submission
JOURNAL Submitted (19-JAN-1999) Clinical Virology, Laboratory Medicine,
Guldhedsgatan 10B, Goreborg 413 46, Sweden
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ORIGIN	PSRRRSQSPRRRSQSRSEQC"	JOURNAL	Submitted (28-JUN-2000) Department of Infectious Disease, Nanfang Hospital, The First Medical College of FUA, Tonghe Road, Guangzhou, Guangdong 510515, P.R. China
Query Match	99.1%; Score 674.6; DB 14; Length 3215;	FEATURES	Location/Qualifiers
Best Local Similarity	99.4%; Pred. No. 7.2e-187;	Source	1..3215
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Query Match	99.1%; Score 674.6; DB 14; Length 3215;
Best Local Similarity	99.4%; Pred No. 7.2e-187;
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QY	1 ATGGAGAACATCGCATCAGGATCTCTAGGACCCCTGCTGCTGTTACAGCGGGGTTTTTC 60
Db	155 ATGGAGAACATCACATCAGGATCTCTAGGACCCCTGCTGCTGTTACAGCGGGGTTTTTC 214
QY	61 TTGTTGACAAAATCCTCAATACCGCAGAGTCTAGACTCTGCTGCTGCTCTCAAT 120
Db	215 TTGTTGACAAAATCCTCAATACCAATACAGATCTAGACTCTGCTGCTCTCAAT 274
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LOCUS	Hepatitis B virus isolate 3c, complete genome.
DEFINITION	
ACCESSION	AF479684
VERSION	AF479684.1 GI:19224211
KEYWORDS	
SOURCE	Hepatitis B virus
ORGANISM	Hepatitis B virus
REFERENCE	Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
AUTHORS	1 (bases 1 to 3215) Huang,W.J., Zhang,H.Y., Wang,Y.C., Wu,X., Gu,W.J., Ling,J.X. and Lan,H.Y.
TITLE	Direct Submission
JOURNAL	Submitted (31-JAN-2002) NO 2 Department of Viral Vaccines, National Institute for the Control of Pharmaceutical and Biological Products, Tiantan Xili 2#, Beijing, P.R. China
FEATURES	Location/Qualifiers

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CDS

ORIGIN

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Query Match          99.1%; Score 674.6; DB 14; Length 3215;
Best Local Similarity 99.4%; Pred. No. 7.2e-187;
Matches 677; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy      1 ATGAGACATCGCATCAGACTCTCTAGGACCCCTGCTGTTTACAGGGGGGTTTTTC 60
Db      155 ATGAGAACATCGCATCAGACTCTCTAGGACCCCTGCTGTTTACAGGGGGGTTTTTC 214

Qy      61 TTGTTGACAAAATCCTCAATACCGCAGAGTCTAGACTCGTGGTGGACTTCTCTCAAT 120
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Db      275 TTCTAGGGGGAACACCCGTGTGTCTTGGCCAAAATTCGCAGTCCCAAAATCTCCAGTCAC 334

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Qy      661 TGTCTTTGGGTATACATTTAA 681
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 26, 2004, 10:52:19 ; Search time 374 Seconds
(without alignments)
7735.355 Million cell updates/sec

Title: US-09-719-533a-1_COPY_155_835
Perfect score: 681
Sequence: 1 ATGGAGACATCGCATCAGG.....GCTCTTGGGTATACATTAA 681

Scoring table: IDENTITY_NUC
Gapop 10_0 , Gapext 1.0

Searched: 3373863 seqs, 212409041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N Geneseq 29Jan04: *
1: Geneseqn1980s: *
2: Geneseqn1990s: *
3: Geneseqn2000s: *
4: Geneseqn2001as: *
5: Geneseqn2001bs: *
6: Geneseqn2002s: *
7: Geneseqn2003as: *
8: Geneseqn2003bs: *
9: Geneseqn2003cs: *
10: Geneseqn2004s: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	681	100.0	3215	3	Aaz29453 Mutant he
2	655.6	96.3	690	2	Aaz29453 Hepatitis
3	649	95.3	687	2	Aaz29453 Hepatitis
4	637.8	93.7	3220	3	Aaz29453 Hepatitis
5	634.8	93.2	684	2	Aaz29453 Hepatitis
6	634.6	93.2	681	2	Aaz29453 Hepatitis
7	634.6	93.2	1170	2	Aaz29453 Hepatitis
8	631.4	92.7	681	1	Aaz29453 Hepatitis
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12	631.4	92.7	756	2	Aaz29453 Hepatitis
13	631.4	92.7	843	2	Aaz29453 Hepatitis
14	631.4	92.7	852	1	Aaz29453 Hepatitis
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16	631.4	92.7	860	1	Aaz29453 Hepatitis
17	631.4	92.7	1161	2	Aaz29453 Hepatitis
18	631.4	92.7	1167	2	Aaz29453 Hepatitis
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21	631.4	92.7	3183	1	Aaz29453 Hepatitis
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ALIGNMENTS

RESULT 1
ID AAZ29453 standard; DNA; 3215 BP.

AC AAZ29453;

DT 06-AUG-2003 (revised)
DT 14-MAR-2000 (first entry)

DE Mutant hepatitis B viral genome.

KW HBIG; Hepatitis B immunoglobulin; HBV; Hepatitis B virus;

KW mutant major surface antigen; human hepatitis B viral genome;

KW human hepatitis B virus surface antigen- 'S'- 145 Singapore strain;

KW hepatocellular carcinoma; HBV infection; circular; cyclic; ds.

OS Hepatitis B virus.

PH Key Location/Qualifiers

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WO9966047-A1.

23-DEC-1999.

19-JUN-1998; 98WO-SG0000045.

19-JUN-1998; 98WO-SG0000045.

(GOVE-) GOVERNMENT REPUBLIC SINGAPORE.

Ocn CJ, Lim GK, Leong AL, Zhao Y, Chen WN;

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DR WPI; 2000-106103/09.
 DR P-PSDB; AAY44348; AAY44349, AAY44350, AAY44351.
 XX New vaccine-escape mutant of hepatitis B virus and related proteins,
 PT nucleic acids and antibodies, useful for diagnosis, prevention and
 PT treatment.
 XX Claim 3; Fig 3; 65pp; English.
 XX The present sequence encodes 4 overlapping reading frames of mutant human
 CC hepatitis B viral genome. This was isolated from a male, 11 year old
 CC Singaporean child which had received standard HBIG and HB vaccine and was
 CC infected with the mutated strain designated human hepatitis B virus
 CC surface antigen- 'S'-145 Singapore strain, a year later. This DNA is
 CC used for recombinant production of mutant major surface antigen and as a
 CC source of diagnostic oligonucleotides. The mutated major surface antigen
 CC is used to raise specific antibodies, to identify specific binding agents
 CC and, in vaccines or compositions for treatment or prevention of HBV
 CC infection and hepatocellular carcinoma. Antibodies are used in diagnosis
 CC or for screening donated body fluids or tissues. (Updated on 06-AUG-2003
 CC to correct OS field.)
 XX Sequence 3215 BP; 736 A; 852 C; 726 G; 901 T; 0 U; 0 Other;
 SQ Query Match 100.0%; Score 681; DB 3; Length 3215;
 Best Local Similarity 100.0%; Pred. No. 4.3e-199;
 Matches 681; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 815 TGTCTTTGGGTATACATTTAA 835
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 DT 16-OCT-2003 (revised)
 DT 25-MAR-2003 (revised)
 DT 19-DEC-1995 (first entry)
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 DE Hepatitis B virus surface antigen protein (HBsAg) isolate 2.
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 KW Hepatitis B virus; surface antigen; envelope region; 'a' determinant; ss.
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 OS Hepatitis B virus; isolate 2.
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 XX
 PI Karayiannis P, Thomas HC;
 XX
 DR WPI; 1995-283727/37.
 XX
 PT New mutant hepatitis B surface antigen - used for the detection
 XX prevention and treatment of hepatitis B infection.
 XX
 PS Claim 10; Fig 7; 39pp; English.
 XX
 CC Two Chinese patients with hepatitis were studied. Patient No. 1 was a 58
 CC year old male, with a 6 year history of non-A, non-B chronic hepatitis.
 CC HBV-DNA was found by PCR in the absence of HBsAg and other HBV markers at
 CC a time when the patient had cirrhosis. Patient No. 2 was a 23 year old
 CC woman from the south of China who on routine testing had a slightly
 CC elevated serum aminotransferase (ALT) level and was positive for HBsAg
 CC and HBeAg, but negative for both immunoglobulin (Ig) M and IgG anti-HBs.
 CC On follow-up she continued to be HBV-DNA positive and was also anti-HBc.
 CC negative but negative for HBsAg, HBeAg and anti-HBs. Both patients were
 CC negative for hepatitis C virus (HVC) and HVC-RNA. DNA was isolated from
 CC serum samples and used as a template for PCR amplification. Primers M3
 CC and 3C (see AAQ98187 & AAQ98188) were used to amplify the Pre-C and C
 CC regions. Direct sequencing of the PCR products was carried out using
 CC sequencing primers AAQ98181-Q98186. The S genes consist of 687 bp in
 CC isolate 1, 690 bp in isolate 2 and 681 bp in the wild types. The S
 CC nucleotide and AA sequences of the mutants were compared with a published
 CC sequence of the same subtype (adw) and also with a wild type strain from
 CC an HBeAg-positive carrier from the same region. Sequencing results
 CC revealed an insertion in the S gene. Inserted sequences encode two
 CC additional AAs (Arg-Ala) between codons 122 and 123 in isolate 1, and
 CC three additional AAs (Arg-Gly-Ala) between codons 123 and 124 in isolate
 CC 2. These insertions occur immediately before the 'a' determinant of
 CC HBsAg. (Updated on 25-MAR-2003 to correct PN field.) (Updated on 16-OCT-
 CC 2003 to standardise OS field)
 XX
 SQ Sequence 690 BP; 140 A; 186 C; 145 G; 219 T; 0 U; 0 Other;
 Query Match 96.3%; Score 655.6; DB 2; Length 690;
 Best Local Similarity 98.1%; Pred. No. 1.5e-191;

Matches	677;	Conservative	0;	Mismatches	4;	Indels	9;	Gaps	1.
QY	1	ATGAGAACATCGCATCAGGACTCCTAGGACCCCCTGCTGTATTACAGCGGGTTTTTC	60						
Ddb	1	ATGAGAACATCAATCAGGACTCCTAGGACCCCCTGCTGTATTACAGCGGGTTTTTC	60						
QY	61	TGTTGCACAAAATCCTCAAAATACCGCAGAGTCTAGACTCGTGGTGGACTTCTCTCAAT	120						
Ddb	61	TGTTGTACAAAAATCCTCAAAATACCACAGAGTCTAGACTCGTGGTGGACTTCTCTCAAT	120						
QY	121	TTTCTAGGGGGAACAACCGGTGTGTCTTGGCCAAAATTCGCAGTCCCAAATCTCCAGTCAC	180						
Ddb	121	TTTCTAGGGGGAACAACCGGTGTGTCTTGGCCAAAATTCGCAGTCCCAAATCTCCAGTCAC	180						
QY	181	TCACCAAGCTTTGTCCTCAATTTGTCCTGGTTATCGCTGGATGTGTCGGGGTTTTT	240						
Ddb	181	TCACCAAGCTTTGTCCTCAATTTGTCCTGGTTATCGCTGGATGTGTCGGGGTTTTT	240						
QY	241	ATCATCTTCCTCTGCATCCCTGCTGTATGCTCATCTTCTTGTTGGTTCTTCTGGACTAT	300						
Ddb	241	ATCATCTTCCTCTGCATCCCTGCTGTATGCTCATCTTCTTGTTGGTTCTTCTGGACTAT	300						
QY	301	CAAGGTATGTTGCCGGTTTGTCTTAATTTCCAGGATCAACAACACCGACCGGACCA	360						
Ddb	301	CAAGGTATGTTGCCGGTTTGTCTTAATTTCCAGGATCAACAACACCGACCGGACCA	360						
QY	361	TGCAAAA-----CCTGCACAACTCTGCTCAAGGAACCTCTATGTTTCCCTCATGT	411						
Ddb	361	TGCAAAAACACGGGGCGCTGCACAACTCTCTCAAGGAACCTCTATGTTTCCCTCATGT	420						
QY	412	TGCTGTACAAACCTACGGACAGAACTGCACCTGTATTCCCATCCATCATCTTGGGCT	471						
Ddb	421	TGCTGTACAAACCTACGGACGGAACCTGCACCTGTATTCCCATCCATCATCTTGGGCT	480						
QY	472	TTCCGAAAATACCTATGGGAGTGGCCCTCAGTCCGTTTCTCTTGGCTCAGTTTACTAGT	531						
Ddb	481	TTCCGAAAATACCTATGGGAGTGGCCCTCAGTCCGTTTCTCTTGGCTCAGTTTACTAGT	540						
QY	532	CCATTTGTTTCAGTGGTTCGTAGGGCTTTCCCCCACTGTCTGGCTTTTCAGTTATATGGATG	591						
Ddb	541	CCAATTGTTTCAGTGGTTCGTAGGGCTTTCCCCCACTGTCTGGCTTTTCAGTTATATGGATG	600						
QY	592	ATGTGGTTTTGGGGGCCAAGTCTGTACAACTCTTGAGTCCCTTTATGCCGCTGTATCCA	651						
Ddb	601	ATGTGGTTTTGGGGGCCAAGTCTGTACAACTCTTGAGTCCCTTTATGCCGCTGTATCCA	660						
QY	652	ATTTCCTTTTGTCTTTGGGTATACATTAA	681						
Ddb	661	ATTTCCTTTTGTCTTTGGGTATACATTAA	690						
RESULT	3:								
ID	AAQ98179	standard; DNA; 687 BP.							
XX	AAQ98179;								
XX	AC								
DT	16-OCT-2003 (revised)								
DT	25-MAR-2003 (revised)								
DT	19-DEC-1995 (first entry)								
DE	Hepatitis B virus surface antigen protein (mHBsag) isolate 1.								
XX	Hepatitis B virus; surface antigen; envelope region; 'a' determinant; ss.								
XW	Hepatitis B virus; isolate 1.								
OS	Hepatitis B virus; isolate 1.								
FH	Key Location/Qualifiers								
FT	variation 367..372								
FT	/tag= a								
FT	/label= insertion								
PN	WO9521189-A1.								

Qy	361	TGCAA-----AACCTGCACAACCTCCTGGCTCAAGAACCTCTATGTTTCCCTCATGTTGC	414
Db	361	TGCAAAACGGGCACCTTCGCACAACTCCTGCTCAAGAACCTCTATGTTTCCCTCATGTTGC	420
Qy	415	TGTACAAAACCTACGGACAGAAAC"TGCAACCTGTATTCCCATCCCATCATCATCTGGGGCTTTC	474
Db	421	TGTACAAAACCTACGGACAGAAAC"TGCAACCTGTATTCCCATCCCATCATCATCTGGCGCTTC	480
Qy	475	GCAAAATACCTATGGAGTGGGCCTCAGTCGCTTCTCTGGGCTCAGTTTACTAGTGCCA	534
Db	481	GCAAAATACCTATGGAGTGGGCCTCAGTCGCTTCTCTGGGCTCAGTTTACTAGTGCCA	540
Qy	535	TTTGTTTCAGTGGTTCGTAGGGCTTTCCGCCCACTGCTGGCTTTACAGTTATATGGATGATG	594
Db	541	TTTGTTTCAGTGGTTCGTAGGGCTTTCCGCCCACTGCTGGCTTTACAGTTAATGAGATGATG	600
Qy	595	TGGTTTTGGGGGCCAAGTCTGTAACAATCTTGAGTCCTCTTATGCCGCTGTATACCAATT	654
Db	601	TGTTTTTGGGGGCCAAGTCTGATCAACATCTTGAGTCCCTTTATGGCGCTGTTACCAATT	660
Qy	655	TTCTTTTGTCTTTGGGTATACATTTAA	681
Db	661	TTCTTTTGTCTTTGGGTATACATTTAA	687

RESULT 4

RESOLUTION #
AAZ88924
ID AAZ88924 standard; DNA; 3220 BP.

XX	
XX	
AC	AZ88924;
XX	
XX	
DT	06-AUG-2003 (revised)
DT	26-MAY-2000 (first entry)
XX	
DE	Hepatitis B virus genomic DNA fragment.
XX	
XX	Detection; PCR; diagnosis; infection; ds
KW	

WPI: 2000-183936/17.

Oligonucleotide primers and probes, for the detection of hepatitis B virus, are used to amplify, by polymerase chain reaction, a section of the hepatitis B virus genome.

Disclosure; Page 8-11; 22pp; German.

This invention describes a novel method of detecting hepatitis B virus (HBV) in a sample which comprises exposing the sample to a polymerase chain reaction (PCR), where the PCR amplified DNA fragment corresponds to part of the HBV genome in the region of positions 242-482 of the HBV genome, counted from the single start cleavage site in the genome. The oligonucleotides and methods are useful for the detection of Hepatitis B virus in samples. This is useful for the diagnosis of chronic Hepatitis B infection. This sequence represents a fragment of the HBV genome described in the method of the invention. (Updated on 06-AUG-2003 to correct OS field.)

Sequence 3220 BP; 733 A; 862 C; 716 G; 909 T; 0 U; 0 Other;

Query Match	93.7%;	Score 537.8;	DB 3;	Length 3220;
Best Local Similarity	96.0%;	Pred. No. 9.1e-186;		
Matches 654;	Conservative 0;	Mismatches 27;	Indels 0;	Gaps 0;
QY	1	ATGAGAGAACATCGCATCAGCACTCCTTAGGACCCCTGCTCGTGTATACAGGGGGGGTTTTTC	60	
DB	156	ATGAGAGAACATCACATCAGGATTCCTTAGGACCCCTGCTCGTGTATACAGGGGGGGTTTTTC	215	
QY	61	TTGTTGACAAAATCCTCACAATACCGCAGAGCTAGACTCTGTTGGTGGACTTCTCTCAAT	120	
DB	216	TTGTTGACAGAATCCTCACAATACCAACAGAGCTAGACTCGTGGTGGACTTCTCTCAAT	275	
QY	121	TTTCTAGGGGGACACCCGGTGCTCTGGGCAAAATTCGCAGTCCCAAAATCTCCAGTCCAC	180	
DB	276	TTTCTAGGGGGACACCCGGTGCTCTGGGCAAAATTCGCAGTCCCAAACTCCATCCAC	335	
QY	181	TCACCAACCTGTTGTCTCCAAATTTGTCCTGGTTATGCTGTGGATGTCTCTGCGGGGTTTT	240	
DB	336	TCACCAACCTTTGTTCTCTCCAACTTGTCCTGGTTATGCTGTGGATGTCTCTGCGGGGTTTT	395	
QY	241	ATCATCTTCCTCTGCATCCGCTGCATGCTCATCTCTTTGTTGGTTCTCTCTGGACTAT	300	
DB	396	ATCATCTTCCTCTGCATCCGCTGCATGCTCATCTCTTTGTTGGTTCTCTCTGGACTAT	455	
QY	301	CAAGGTATGTTGCCGGTTTGCTCTTAATTCAGGATCAACAACACCGACACCGGACCA	360	
DB	456	CAAGGTATGTTGCCGGTTTGCTCTTAATTCAGGATCATCAACACCGACACCGGACCA	515	
QY	361	TGCBAACCTGCGACACTCCCTGCTCAAGGAACCTCTATGTTTCCCTCATGTTGCTGTACA	420	
DB	516	TGCBAACCTGCGACGACTCTCTGCTCAAGGAACCTCTATGTTTCCCTCTGTTGCTGTACA	575	
QY	421	AAACCTACGGACAGAAACTGCACCTGTATTCCCATCCCATCATCTTTGGGCTTTCCGCAAA	480	
DB	576	AAACCTTCGGACGGAAACTGCACCTGTATTCCCATCCCATCATCTTTGGGCTTTCCGCAAA	635	
QY	481	TACCTATGGAGTGGGGCTCAGTCCGTTTCTCTTGCTCAGTTTACTAGTGCCATTTGTT	540	
DB	636	TTCTATGGAGTGGGGCTCAGTCCGTTTCTCTTGCTCAGTTTACTAGTGCCATTTGTT	695	
QY	541	CAGTGGTTCTGATAGGGCTTTCCCCCACTGCTGCTCTTTCAGTTATATGGATGATGTGGTTT	600	
DB	696	CAGTGGTTCTGATAGGGCTTTCCCCCACTGTTTGCCTTTCAGTTATATGGATGATGTGGTAT	755	
QY	601	TGGGGGCCAAGTCTGTACAACATCTTGAGTCCCTTTATGCGCGCTGTACCAATTTCTTT	660	
DB	756	TGGGGGCCAAGTCTGTACAGCATCTTGAGTCCCTTTTACCOCCTGTGTACCAATTTCTTT	815	
QY	661	TGTCCTTTGGGTATACATTTAA	681	
DB	816	TGCTTTGGGTATACATTTAA	836	

RESULT 5

AAQ75318

ID AAQ75318 standard; DNA: 684 BP.

RESIT.T 5

RESULT 3
AAQ75318
ID AAQ75318 standard; DNA: 684 BP.

AAQ75318;
AC
XX
XX
XX
DT
DT
XX
XX
DE
XX
XX
KW
KW
KW
XX
OS
XX
XX
FH
FT
FT

FT		/transl_except= AAC encodes Threonine.	
FT	misc_difference	289..291	
FT		*tag= b	
FT	/transl_except= COT encodes Leucine.		
FT	insertion_seq	367..372	
FT		*tag= c	
XX			
PN	WO9426904-Al.		
PN			
XX			
PD	24-NOV-1994.		
XX			
XX	09-MAY-1994;	94WO-US005090.	
Pf			
PF	07-MAY-1993;	93US-00059031.	
XX	(ABBO) ABBOTT LAB.		
PA	(UNITU) UNIV GLASGOW.		
PA			
XX	Carman W, Decker RH, Wallace L, Mimms LT, Solomon LR;		
PI			
PI			
XX			
DR	WPI; 1995-006799/01.		
DR	P-PSDB; AAR67368.		
XX			
XX	New mutant hepatitis B virus polynucleotide - used to develop prods. for		
PT	diagnosis, prognosis, therapy and studies involving hepatitis B		
PT	infection.		
XX			
XX	Example 2; Page 48-49; 59pp; English.		
PS			
XX	The mutant hepatitis B virus (HBV) polynucleotide comprises an insertion		
CC	of six nucleotides at position 366 of the HBV surface antigen (HBSAg)		
CC	gene. The polynucleotide can be used for detection of mutant HBV and for		
CC	the production of mutant polypeptides which can be used in vaccines for		
CC	the treatment of infection. Antibodies against such polypeptides can be		
CC	used for detecting the mutant HBV antigen. (Updated on 25-MAR-2003 to		
CC	correct PN field.)		
XX			
SQ	Sequence 684 BP; 140 A; 189 C; 142 G; 213 T; 0 U; 0 Other;		
	Query Match	93.2%; Score 634.8; DB 2; Length 684;	
	Best Local Similarity	96.6%; Pred. No. 3.8e-185;	
	Matches 661; Conservative 0; Mismatches 17; Indels 6; Gaps 1;		
QY	1 ATGGAGAACATCGCATCAGGAACCTCTAGGACCCTCTAGGACCCTCTGTCTTACAGGCGGGTTTC 60		
Db	1 ATGGAGAACACCAATCAGGACTCTAGGACCCTCTAGGACCCTCTGTCTTACAGGCGGGTTTC 60		
QY	61 TTGTTGACAAAATCCTCACATACCGCAGAGTCTAGAGTCTGTGTGAGTCTCTCAAT 120		
Db	61 TTGTTGACAAAATCCTCACATACCGCAGAGTCTAGAGTCTGTGTGAGTCTCTCAGT 120		
QY	121 TTTTAGGGGAAACCCCGTGCTGTGTCGCCAAAATTCCGAGTCCCAAATCTCCAGTCAC 180		
Db	121 TTTTAGGGGAAACCCCGTGCTGTGTCGCCAAAATTCCGAGTCCCAAATCTCCAGTCAC 180		
QY	181 TCACCAACTGTGTCTTCCAATTTGCTGTGTTATCGCTGATGTCTCGGCGTTTT 240		
Db	181 TCACCAAACTGTGTCTTCCAATTTGCTGTGTTATCGCTGATGTCTCGGCGTTTT 240		
QY	241 ATCATCTTCTCTGCATCTCTGCTGTGTCCTCATCTTCTTGTGTTCTTCTGCATAT 300		
Db	241 ATCATCTTCTCTGCATCTCTGCTGTGTCCTCATCTTCTTGTGTTCTTCTGCATAT 300		
QY	301 CAAGGTATGTCGCCGTTTGTCTCTTAATTCAGGATCAACAACACGACCGGACCA 360		
Db	301 CAAGGTATGTCGCCGTTTGTCTCTTAATTCAGGATCAACAACACGACCGGACCA 360		
QY	361 TG-----CAAACTGCAACTCTCTGCTCAAGAACCTCTATGTTTCCCTCATGTTGC 414		
Db	361 TGCAAGAACACAACTCTGCTGCTCAAGAACCTCTATGTTTCCCTCATGTTGC 420		
QY	415 TGTACAAAACCTACGACAGAAACTGCACCTGTATTCCTATCCCATCATCTTGGGCTTTC 474		

Db 1030 CAGTGGTTCGAGGCTTCCCCACTGTTGGCTTTCAGCTATATGATGATGAT 1089
Qy 601 TGGGGCCCAAGTCTGTACAAATCTTGAGTCCCTTTATGCGCTGTACCAATTTCTTT 660
Db 1090 TGGGGCCCAAGTCTGTACAGCATCGTGAATCCCTTTATACCGCTGTACCAATTTCTTT 1149
Qy 661 TGTCTTTGGGTATACATTAA 681
Db 1150 TGTCTCTGGGTATACATTAA 1170

RESULT 8
AAN60152
ID AAN60152 standard; DNA; 681 BP.
XX AAN60152;
XX
DT 25-MAR-2003 (revised)
DT 24-AUG-1991 (first entry)
XX
DE Sequenc encoding adw type hepatitis B virus (HBV).
XX
XX Vaccine; hepatitis B virus; antigen; ss.
XX
OS Hepatitis B virus.
XX
XX
FH Key Location/Qualifiers
FT CDS 1..681
FT /*tag= a

EP175283-A.
XX
XX
XX 26-MAR-1986.
XX
XX 12-SEP-1985; 85EP-00111530.
XX
XX 13-SEP-1984; 84JP-00193765.
XX
XX (TAKE) TAKEDA CHEM IND LTD.
XX
XX Kikuchi M, Fujisawa Y;
XX
XX WFI; 1986-083075/13.
DR P-PSDB; AAP60223.

XX
XX Recombinant DNA contg. gene for hepatitis B surface antigen - and
PT sequence complementary for 18S ribosomal RNA, and new yeast
PT transformants.
XX
XX Disclosure; Fig 1; 29pp; English.

XX
XX The pref. DNA coding for the surface antigen of adw type hepatitis B
CC virus is AAN60152. The recombinant DNA of the invention (see PT) is used
CC to transform yeast cells to produce HBSAg in quantities sufficient for
CC making vaccines. (Updated on 25-MAR-2003 to correct PA field.)
XX
XX Sequence 681 BP; 139 A; 182 C; 142 G; 218 T; 0 U; 0 Other;

SQ
Qy 1 ATGGAGACATCGCATCAGGACCTCTAGGACCCCTCTCGTGTACAGGCGGGTTTTC 60
Db 1 ATGGAGAACATCATCATCAGGATTCCTTAGGACCCCTCTCGTGTACAGGCGGGTTTTC 60
Qy 61 TTGTTGACAAAATTCCTCACAATACCGCAGAGTCTAGACTCGTGGTGGACTTCTCTCAAT 120
Db 61 TTGTTGACAGAAATTCCTCACAATACCGCAGAGTCTAGACTCGTGGTGGACTTCTCTCAAT 120
Qy 121 TTCTAGGGGAAACACCCCGTGTCTTGGCCAAAATTCGAGTCCCAATCTCCAGTCAC 180

Query Match 92.7%; Score 631.4; DB 1; Length 681;
Best Local Similarity 95.4%; Pred. No. 4.2e-184;
Matches 650; Conservative 0; Mismatches 31; Indels 0; Gaps 0;
Qy 1 ATGGAGACATCGCATCAGGACCTCTAGGACCCCTCTCGTGTACAGGCGGGTTTTC 60
Db 1 ATGGAGAACATCATCATCAGGATTCCTTAGGACCCCTCTCGTGTACAGGCGGGTTTTC 60
Qy 61 TTGTTGACAAAATTCCTCACAATACCGCAGAGTCTAGACTCGTGGTGGACTTCTCTCAAT 120
Db 61 TTGTTGACAGAAATTCCTCACAATACCGCAGAGTCTAGACTCGTGGTGGACTTCTCTCAAT 120
Qy 121 TTCTAGGGGAAACACCCCGTGTCTTGGCCAAAATTCGAGTCCCAATCTCCAGTCAC 180

Db 121 TTTCTAGGGGATCACCCGTGTCTTTGGCCAAAATTCGAGTCCCAACCTCCCAATCAC 180
Qy 181 TCACCAACCTGTTGTTCTTCCAAATTTGCTCTGGTTATCGCTGGATGTTCTGCGCGTTTT 240
Db 181 TCACCAACCTGTTGTTCTTCCAAATTTGCTCTGGTTATCGCTGGATGTTCTGCGCGTTTT 240
Qy 241 ATCATCTTCTCTGCAATCTGCTGTATGCTCATCTTCTTGTGTTCTTCTTGGACTAT 300
Db 241 ATCATATTCCTTCTCATCTGCTGTATGCTCATCTTCTTGTGTTCTTCTTGGACTAT 300
Qy 301 CAAAGGTATGTTGCCGTTTCTCTTAATTCAGGATCAACAACAACAGTACGGGACCA 360
Db 301 CAAAGGTATGTTGCCGTTTCTCTTAATTCAGGATCAACAACAACAGTACGGGACCA 360
Qy 361 TGCAAAAACCTGCAACCTCTGCTCAAGGAACCTCTATGTTTCCCTCATGTTGCTGTACA 420
Db 361 TGCAAAAACCTGCAACCTCTGCTCAAGGAACCTCTAAAGTTTCCCTCATGTTGCTGTACA 420
Qy 421 AAACCTACGGATGGAATTTGACCTGTATTCCTTCCCATCCATCGTCTGGGTTTCGCAAAA 480
Db 421 AAACCTACGGATGGAATTTGACCTGTATTCCTTCCCATCCATCGTCTGGGTTTCGCAAAA 480
Qy 481 TACCTATGGAGTGGGCTCAGTCCGTTTCTTTGGCTCAGTTTACTAGTGCCATTGTT 540
Db 481 TACCTATGGAGTGGGCTCAGTCCGTTTCTTTGGCTCAGTTTACTAGTGCCATTGTT 540
Qy 541 CAGTGGTTCGTAGGGCTTTCCCACTGTCTGCTTCCCTTATGCTATATGATGATGTT 600
Db 541 CAGTGGTTCGTAGGGCTTTCCCACTGTCTGCTTCCCTTATGCTATATGATGATGTT 600
Qy 601 TGGGGGCAAGTCTGTATCAACATCTTGAGTCCCTTTATGCGCTGTATACCAATTTCTTT 660
Db 601 TGGGGGCAAGTCTGTATCAACATCTTGAGTCCCTTTATGCGCTGTATACCAATTTCTTT 660
Qy 661 TGTCTTGGGTATACATTAA 681
Db 661 TGTCTTGGGTATACATTAA 681

RESULT 9
AAN80974
ID AAN80974 standard; DNA; 681 BP.
XX
XX AAN80974;
XX
DT 27-AUG-2003 (revised)
DT 25-MAR-2003 (revised)
DT 21-JAN-1991 (first entry)
XX
XX Sequence encoding S protein having hepatitis B virus (HBV) surface
DE antigen (HBSAg) activity.
XX
XX Egg white lysozyme; hepatitis B virus (HBV) surface antigen (HBSAg);
KW Saccharomyces cerevisiae AH228/PGLD LP39-Rct;
KW Saccharomyces cerevisiae L11P39-Rct; Saccharomyces cerevisiae LP31-Rct;
KW protein secretion; ss.
XX
XX Hepatitis B virus.
XX
FH Key Location/Qualifiers
FT CDS 1..681
FT /*tag= a
XX
XX EP288198-A.
XX
PD 26-OCT-1988.
XX
XX 13-APR-1988; 88EP-00303297.
XX
XX 20-APR-1987; 87JP-00098265.
PR 12-OCT-1987; 87JP-00256885.
PR 18-APR-1988; 88JP-00095335.
XX

QY 301 CAAGGTATGTCGCCGTTGTCCTCTAATTCAGGATCAAAACACAGCAGCGACCA 360
Db 301 CAAGGTATGTCGCCGTTGTCCTCTAATTCAGGATCAAAACACAGCAGCGACCA 360
QY 361 TCGAAACCTGCACAACTCTCTCTCAAGAACTCTATGTTTCCCTCTATGTTGCTGTACA 420
Db 361 TCGAAACCTGCACAACTCTCTCTCAAGAACTCTATGTTTCCCTCTATGTTGCTGTACA 420
QY 421 ARAACTACGGACAGAACTGCACCTGTATTCCCATCCCATCATCTTGGCTTTGSCAAA 480
Db 421 ARAACTACGGACAGAACTGCACCTGTATTCCCATCCCATCATCTTGGCTTTGSCAAA 480
QY 481 TACCTATGGAGTGGGCTCTAGTCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 540
Db 481 TACCTATGGAGTGGGCTCTAGTCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 540
QY 541 CAGTGGTTCGTAGGGCTTTCCGCCACTGCTGGCTTCAGTTATATGATGATGTTT 600
Db 541 CAGTGGTTCGTAGGGCTTTCCGCCACTGTTGGCTTCAGTTATATGATGATGTTT 600
QY 601 TGGGGGCCAAGTCTGTACAACTCTAGTCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 660
Db 601 TGGGGGCCAAGTCTGTACAACTCTAGTCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 660
QY 661 TGTCTTTGGGTATACATTTAA 681
Db 661 TGTCTCTGGGTATACATTTAA 681

RESULT 11
ID AAN70247
XX AAN70247 standard; DNA; 690 BP.
XX AAN70247;
XX AAN70247;
DT 24-OCT-2003 (revised)
DT 03-APR-1991 (first entry)
XX DE Hybrid sequence of Pichia pastoris regulatory region and hepatitis B
XX DE surface antigen coding region.
XX DE
XX KW Hepatitis B virus antigen; vaccine; ss.
XX OS Pichia pastoris; and hepatitis B virus.
XX PN EP226846-A.
XX PD 01-JUL-1987.
XX PF 25-NOV-1986; 86EP-00116302.
XX PR 26-NOV-1985; 85US-00801713.
XX PA (PHIP) PHILLIPS PETROLEUM CO.
XX PI Teschopp JF, Harpold MM, Gregg JM, Buckholz RG;
XX WI; 1987-179248/26.
XX PT Yeast prodn. of hepatitis B surface antigen - with regulatory regions
XX PT responsive to methanol non-catabolite repressing carbon source or carbon
XX PT source starvation.
XX PS Claim 5; p21; 33pp; English.
XX CC The regulatory region is derived from the dihydroxyacetone synthase (DAS)
XX CC gene of Pichia pastoris, from the primary alcohol oxidase (AOXI) gene of
XX CC P. pastoris or from the p40 gene of P. pastoris. Using AAN70247, HBsAg
XX CC can be produced in high yealds. (Updated on 24-OCT-2003 to standardise OS
XX CC field)
XX SQ Sequence 690 BP; 139 A; 184 C; 145 G; 222 T; 0 U; 0 Other;

Query Match 92.7%; Score 631.4; DB 1; Length 690;
Best Local Similarity 95.4%; Pred. No. 4.2e-184;
Matches 650; Conservative 0; Mismatches 31; Indels 0; Gaps 0;
QY 1 ATGAGAACATCGCATCAGACTCCCTAGGACCCCTGCTGCTGTACAGGCGGGTTTTC 60
Db 7 ATGAGAACATCATCAGGATTCCTAGGACCCCTGCTGCTGTACAGGCGGGTTTTC 66
QY 61 TTGTTGACAAAAATCCCTCACAATACCGCAGAGTCTAGACTCGTGGTGGACTTCTCTCAAT 120
Db 67 TTGTTGACAAAGATCCCTCACAATACCGCAGAGTCTAGACTCGTGGTGGACTTCTCTCAAT 126
QY 121 TTCTAGGGGGAACACCCGCTGTCTTGGCCAAAATTCGAGTCCCAAAATCTCCAGTAC 180
Db 127 TTCTAGGGGGAATCTCCCGTGTCTTGGCCAAAATTCGAGTCCCAAAATCTCCAGTAC 186
QY 181 TCACCAACCTGTTGCTCTCCAAATTTGCTGGTATATCGCTGGATGTCTCTCGGCGTTTT 240
Db 187 TCACCAACCTGCTCTCTCCAAATTTGCTGGTATATCGCTGGATGTCTCTCGGCGTTTT 246
QY 241 ATCATCTCTCTCTGCTCTGCTGTATGCTCATCTCTCTCTCTCTCTCTCTCTCTCTCT 300
Db 247 ATCATATTTCTCTCTCTGCTCTGCTGTATGCTCATCTCTCTCTCTCTCTCTCTCTCT 306
QY 301 CARGGTATGTGCCCGTTTGTCTCTAATTCAGGATCAAAACACAGCAGCGGACCA 360
Db 307 CARGGTATGTGCCCGTTTGTCTCTAATTCAGGATCAAAACACAGCAGCGGACCA 366
QY 361 TGCAAAACCTGCACAACTCTCTGCTCAAGGAACTCTATGTTTCCCTCATGTTGCTGTACA 420
Db 367 TGCAAAACCTGCACAACTCTCTGCTCAAGGAACTCTATGTTTCCCTCATGTTGCTGTACA 426
QY 421 AAACCTAGGACAGAACTGCACCTGTATTCGATCCCATCATCTGCGGCTTTCGCAAAA 480
Db 427 AAACCTAGGATGGAAATTCGACCTGTATTCGATCCCATCATCTGCGGCTTTCGCAAAA 486
QY 481 TACCTATGGAGTGGGCTCTAGTCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 540
Db 487 TACCTATGGAGTGGGCTCTAGTCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 546
QY 541 CAGTGGTTCGTAGGGCTTTCCGCCACTGCTGGCTTCAGTTATATGATGATGTTT 600
Db 547 CAGTGGTTCGTAGGGCTTTCCGCCACTGTTGGCTTCAGTTATATGATGATGTTT 606
QY 601 TGGGGGCCAAGTCTGTACAACTCTAGTCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 660
Db 607 TGGGGGCCAAGTCTGTACAACTCTAGTCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 666
QY 661 TGTCTTTGGGTATACATTTAA 681
Db 667 TGTCTCTGGGTATACATTTAA 687

RESULT 12
ID AAO11323
XX AAO11323 standard; DNA; 756 BP.
XX AC AAO11323;
XX XX
DT 27-AUG-2003 (revised)
DT 25-MAR-2003 (revised)
DT 10-JUN-1991 (first entry)
XX XX
DE RP135/HBsAg.
XX KW HIV; envelope; AIDS; ARC; hepatitis; fusion; vaccine; antibodies; ss.
XX OS Hepatitis B virus.
XX OS Synthetic.
XX XX
XX Key Location/Qualifiers
XX CDS 1..75
XX PT /*tag= a

CC polypeptides corresp. to all or part of a protein having the biological
CC activity of one of the hepatitis B surface antigens. The composite
CC particles are useful for preparing improved hepatitis B vaccines or for
CC treating of HBV. See also AAQ10677-79. (Updated on 25-MAR-2003 to correct
CC PA field.) (Updated on 25-MAR-2003 to correct PI field.)
XX
SQ Sequence 843 BP; 174 A; 229 C; 179 G; 261 T; 0 U; 0 Other;

Query Match 92.7%; Score 631.4; DB 2; Length 843;
Best Local Similarity 95.4%; Pred. No. 4.7e-184;
Matches 650; Conservative 0; Mismatches 31; Indels 0; Gaps 0;
QY 1 ATGGAGAACATCGCATCAGGACTCTAGGACCCCTGCTGTTACAGCGGGGTTTTTC 60
Db 163 ATGGAGAACATCAGATCAGGATCTTAGGACCCCTGCTGTTACAGCGGGGTTTTTC 222
QY 61 TTGTTGACAAAATCCTCAATACCGCAGAGCTAGACCTGCTGTTGAGCTTCTCAAT 120
Db 223 TTGTTGACAAAATCCTCAATACCGCAGAGCTAGACCTGCTGTTGAGCTTCTCAAT 282
QY 121 TTTCTAGGGGACACCCGCTGCTTGGCCAAATTCGACATCCCAATCTCCAGTCAC 180
Db 283 TTTCTAGGGGATCACCCTGCTGTTGGCCAAATTCGACATCCCAATCTCCAGTCAC 342
QY 181 TCACCAACCTGTTGCTCTCCAAATTTGCTGTTATCGCTGATGCTGCGGGTTTTT 240
Db 343 TCACCAACCTGTTGCTCTCCAAATTTGCTGTTATCGCTGATGCTGCGGGTTTTT 402
QY 241 ATCACTTCTCTGATCTGCTGCTATGCTCATCTTCTTCTGTTCTTCTGACTAT 300
Db 403 ATCATATCTCTTCTATCTGCTGCTATGCTCATCTTCTTCTGTTCTTCTGACTAT 462
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QY 541 CAGTGTTCGTAGGGCTTTCCGCTTTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 600
Db 703 CAGTGTTCGTAGGGCTTTCCGCTTTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 762
QY 601 TGGGGGCAAGTCTGTACAACTCTTGGAGTCCCTTTATGCTGCTGCTGCTGCTGCTGCT 660
Db 763 TGGGGGCAAGTCTGTACAACTCTTGGAGTCCCTTTATGCTGCTGCTGCTGCTGCTGCT 822
QY 661 TGCTTTGGGTATACATTTAA 681
Db 823 TGCTTTGGGTATACATTTAA 843

RESULT 14
AAN93424
ID AAN93424 standard; DNA; 852 BP.
XX
AC AAN93424;
XX
AC AAN93424;
XX
AC AAN93424;
DT 25-MAR-2003 (revised)
DT 05-APR-1990 (first entry)
XX
DE Sequence of hepatitis B virus preS2 sequence.
XX
KW Hepatitis B virus; preS2 protein; S protein; vaccine.

Hepatitis B virus.
XX
OS
XX
FH Key Location/Qualifiers
FT CDS 7
FT /*tag= a
FT /note= "start of preS2 protein"
FT 172
FT /*tag= b
FT /note= "start of S protein"
XX
PN EP341746-A.
XX
PD 15-NOV-1989.
XX
PE 13-MAY-1988; 88US-00193714.
XX
PR 13-MAY-1988; 88US-00193714.
XX
PA (PHIP) PHILLIPS PETROLEUM CO.
PA (RESE) RESEARCH CORP TECHNOLOGIES INC.
XX
PI Thill GP;
XX
XX
DR WPI; 1989-334102/46.
XX
XX
PT Expression of hepatitis B S and preS2 proteins in methylotrophic yeast -
PT used to obtain antigenic hepatitis B virus particles in more vaccine-
PT effective form.
XX
PS Disclosure; Table 1; 36pp; English.
XX
CC An expression cassette contg. the preS2 gene, and an expression cassette
CC contg. the S gene are used to transform a methylotrophic yeast, to produce
CC antigenic HBV particles which combine the major S protein with the more
CC potentially antigenic preS2 protein. This particle is in a more effective
CC vaccine form. (Updated on 25-MAR-2003 to correct PA field.) (Updated on
CC 25-MAR-2003 to correct PI field.)
XX
SQ Sequence 852 BP; 175 A; 235 C; 182 G; 260 T; 0 U; 0 Other;
Query Match 92.7%; Score 631.4; DB 1; Length 852;
Best Local Similarity 95.4%; Pred. No. 4.7e-184;
Matches 650; Conservative 0; Mismatches 31; Indels 0; Gaps 0;
QY 1 ATGAGAACATCGCATCAGGACTCTAGGACCCCTGCTGTTACAGCGGGGTTTTTC 60
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Db 472 CAGGTATGTTGCCGCTTGTCTCTTAATTCAGGATCAACAAACAGCAGCGGACCA 531
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QY 421 AAACCTACGGACAGAAATGCACTGTATTCCTCCATCCCATCATCTTGGGCTTTTCGAAAA 480
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QY 481 TACATATGGAGTGGGCTCAGTCCGTTTCTCTGGCTCAGTTTACTAGTGCATTTGTT 540
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QY 541 CAGTGGTTCGTAGGGCTTTCCCCACACTGCTGGCTTTTCACTATATGGATGATGTTT 600
Db 712 CAGTGGTTCGTAGGGCTTTCCCCACACTGCTGGCTTTTCACTATATGGATGATGTTT 771
QY 601 TGGGGCCAAAGTCTGTACAGATCGTGAGTCCCTTTATACCGCTGTTACCAATTTTCTTT 660
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QY 661 TGTCTTTGGGTATACATTTAA 681
Db 832 TGTCTTTGGGTATACATTTAA 852

RESULT 15
AAN91823
ID AAN91823 standard; DNA; 859 BP.
AC AAN91823;
XX
DT 22-MAR-1990 (first entry)
DE Pre-S2 structural gene.
DE
DE
XX Antigen.
XX
XX Hepatitis B virus.
XX
XX Key Location/Qualifiers
XX mat_peptide 7..852
XX /*tag= a
XX /note= "pre-S2 protein"
XX mat_peptide 172..852
XX /*tag= b
XX /note= "S protein"
XX
XX EP339567-A.
XX
XX
XX 02-NOV-1989.
XX
XX 25-APR-1989; 89EP-00107457.
XX
XX 25-APR-1988; 88US-00186421.
XX
XX (PHIP ) PHILLIPS PETROLEUM CO.
XX
XX Thill GP;
XX
XX WPI; 1989-317441/44.
XX
XX P-PSDB; AAP93168.
XX
XX Expression of hepatitis B Pres2 protein - in methylotrophic yeast, e.g.
XX Fichla pastoris.
XX
XX Disclosure; Page 5-6; 22pp; English.
XX
XX Pres2 is present in HBV viral coat protein with S and Pres1. In the
XX patent it is used recombinantly to produce antigenic particles for
XX vaccine
XX
XX Sequence 859 BP; 178 A; 238 C; 182 G; 261 T; 0 U; 0 Other;

Query Match 92.7%; Score 631.4; DB 1; Length 859;
Best Local Similarity 95.4%; Pred. No. 4.7e-184;
Matches 650; Conservative 0; Mismatches 31; Indels 0; Gaps 0;

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QY 1 ATGGAGAACATCGCATCAGGACTCCTAGGACCCCTGCTCGTGTACAGGCGGGCTTTTTC 60
Db 172 ATGGAGAACATCACAATCAGGATTCCTAGGACCCCTGCTCGTGTACAGGCGGGCTTTTTC 231
QY 61 TTGTTGACAAAAATCTCTCACAATACCGCAGAGTCTAGACTCGTGGTGGACTTCTCTCAAT 120
Db 232 TTGTTGACAGAAATCTCTCACAATACCGCAGAGTCTAGACTCGTGGTGGACTTCTCTCAAT 291
QY 121 TTTCTAGGGGAAACACCGCTGTCTTTGGCCAAAATTCGACAGTCCGAAATCTCCAGTCAC 180
Db 292 TTTCTAGGGGAAATCTCCCGTGTCTTTGGCCAAAATTCGACAGTCCGAAATCTCCAGTCAC 351
QY 181 TCACCAACCTCTGTCCTCCCAATTTGCTCGTGGTATCGCTGGATGCTCTGCGCGCTTTT 240
Db 352 TCACCAACCTCTGTCCTCCCAATTTGCTCGTGGTATCGCTGGATGCTCTGCGCGCTTTT 411
QY 241 ATCATCTTCTCTGCTATGCTGCTATGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 300
Db 412 ATCATATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 471
QY 301 CAAGTATGTTGCCCGTTTGTCTCTAAATTCAGGATCAACAAACACGACGACGACCA 360
Db 472 CAAGTATGTTGCCCGTTTGTCTCTAAATTCAGGATCAACAAACACGACGACGACCA 531
QY 361 TGCAAAACCTGCAACAATCTCTGCTCAAGGAACTCTATGTTTCCCTCATGTTGCTGTACA 420
Db 532 TGCAAAACCTGCAACAATCTCTGCTCAAGGAACTCTATGTTTCCCTCATGTTGCTGTACA 591
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Db 592 AARCTACGGATGGAATTCGACCTGTATTCCTCCATCCCATCATCTTGGGCTTTTCGCAAA 651
QY 481 TACCTATGGAGTGGGCTCAGTCCGTTTCTCTTGGCTCAGTTTACTAGTGCATTTGTT 540
Db 652 TACCTATGGAGTGGGCTCAGTCCGTTTCTCTTGGCTCAGTTTACTAGTGCATTTGTT 711
QY 541 CAGTGGTTCGTAGGGCTTTCCCCACACTGCTGGCTTTCAGTTATATGGATGATGTTT 600
Db 712 CAGTGGTTCGTAGGGCTTTCCCCACACTGTTGGCTTTCAGTTATATGGATGATGTTT 771
QY 601 TGGGGCCAAAGTCTGTACAAACATCTTGAGTCCCTTTTATGCCGCTGTATCCAAATTTCTTT 660
Db 772 TGGGGCCAAAGTCTGTACAAACATCTTGAGTCCCTTTTATGCCGCTGTATCCAAATTTCTTT 831
QY 661 TGTCTTTGGGTATACATTTAA 681
Db 832 TGTCTTTGGGTATACATTTAA 852

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Search completed: July 26, 2004, 13:54:59

Job time : 377 secs

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OM nucleic - nucleic search, using sw model

Run on: July 26, 2004, 13:25:54 ; Search time 78 Seconds
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Title: US-09-719-533A-1_COPY_155_835
Perfect score: 681
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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5	634.8	93.2	684	1	US-08-447-591-1
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45	615.4	90.4	846	6	5164485-1

ALIGNMENTS

RESULT 1
US-08-500-914A-7
; Sequence 7, Application US/08500914A
; Patent No. 5856084
; GENERAL INFORMATION:
; APPLICANT: KARAVIANNIS, PETER
; APPLICANT: THOMAS, HOWARD C.
; TITLE OF INVENTION: HEPATITIS B VACCINE
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHUYE P.C.
; STREET: 1100 NORTH GLEBE ROAD, 8TH FLOOR
; CITY: ARLINGTON
; STATE: VIRGINIA
; COUNTRY: U.S.A.
; ZIP: 22201-4714
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/500,914A
; FILING DATE: 28-DEC-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: MITCHARD, LEONARD C.
; REGISTRATION NUMBER: 29,009
; REFERENCE/DOCKET NUMBER: 1208-17
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-816-4000
; TELEFAX: 703-816-4100
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 681 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-500-914A-7

Query Match 98.4%; Score 669.8; DB 2; Length 681;
Best Local Similarity 99.0%; Pred. No. 1.1e-200;
Matches 674; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
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Db 1 ATGGAGACATCGCATCAGGACTCTAGACCCCTGCTCGTGTACAGCGGGGTTTTTC 60
QY 61 TTGTTGACAAAAATCCTCACATACCGCAGAGTCTAGACTCGTGTGGACTTCTCTCAAT 120


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Db
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Db
661 TTCTTTTGTCTTTGGGTATACATT 684

RESULT 5
US-08-447-591-1
; Sequence 1, Application US/08447591
; Patent No. 5591440
; GENERAL INFORMATION:
; APPLICANT: CARMAN, WILLIAM
; APPLICANT: DECKER, RICHARD H
; APPLICANT: WALLACE, LESLEY
; APPLICANT: MIMMS, LARRY T
; APPLICANT: SOLOMON, LARRY R
; TITLE OF INVENTION: HEPATITIS B VIRUS MUTANTS, REAGENTS AND METHODS FOR DETECTION
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ABBOTT LABORATORIES D377/AP6D
; STREET: ONE ABBOTT PARK ROAD
; CITY: ABBOTT PARK
; STATE: IL
; COUNTRY: USA
; ZIP: 60064-3500
; COMPUTER READABLE FORM: disk
; MEDIUM TYPE: Floppy
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/447,591
; FILING DATE: 23-MAY-1995
; CLASSIFICATION: 435
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: US 08/059,031
; FILING DATE: 07-MAY-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: FOREMSKI, PRISCILLA E.
; REGISTRATION NUMBER: 33,207
; REFERENCE/DOCKET NUMBER: 5347.US.01
; TELEPHONE: 708-937-6365
; TELEFAX: 708-938-2623
; INFORMATION FOR SEQ ID NO: 1:
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SEQUENCE CHARACTERISTICS:
LENGTH: 684 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 1..684
US-08-447-591-1

Query Match 93.2%; Score 634.8; DB 1; Length 684;
Best Local Similarity 96.6%; Pred. No. 1.1e-189;
Matches 561; Conservative 0; Mismatches 17; Indels 6; Gaps 1;

Qy 1 ATGGAGAACATCGCATCAGGACTCTCTAGGACCCCTGCTGTTTACAGGGGGGTTTTTC 60
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Db 121 TTTCTAGGGGGAACACCCCGTGTCTTGGCCAAATTCGCAGTCCCAATCTCCAGTCAC 180
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Db 301 CAAGGTATGTTGGCGGTTTGTCTTAATTCAGGATCAACAACACGACCGGACCA 360
Qy 361 TG-----CAAACTGCACAACCTCTGCTCAAGGAACCTCTATGTTTCCCTCATGTTGC 414
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Qy 415 TGTACAAACCTACGACAGAACTGCACCTGTATTCCTTGGCTCAGTTTACTAGTGCCA 474
Db 421 TGTACAAACCTACGACAGAACTGCACCTGTATTCCTTGGCTCAGTTTACTAGTGCCA 480
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Qy 655 TTCTTTTGTCTTTGGGTATACATT 678
Db 661 TTCTTTTGTCTTTGGGTATACATT 684

RESULT 6
US-08-450-943-1
; Sequence 1, Application US/08450943
; Patent No. 5593825
; GENERAL INFORMATION:
; APPLICANT: CARMAN, WILLIAM
; APPLICANT: DECKER, RICHARD H
; APPLICANT: WALLIS, LESLEY
; APPLICANT: MIMMS, LARRY T
```

APPLICANT: SOLOMON, LARRY R
TITLE OF INVENTION: HEPATITIS B VIRUS MUTANTS, REAGENTS AND METHODS FOR
DETECTION
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: ABBOTT LABORATORIES D377/AP6D
STREET: ONE ABBOTT PARK ROAD
CITY: ABBOTT PARK
STATE: IL
COUNTRY: USA
ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/450,943
FILING DATE:
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: FOREMSKI, PRISCILLA E.
REGISTRATION NUMBER: 33,207
REFERENCE/DOCKET NUMBER: 5347.US.01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 708-937-6365
TELEFAX: 708-938-2623
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 684 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 1..684
US-08-450-943-1

Query Match 93.2%; Score 634.8; DB 1; Length 684;
Best Local Similarity 96.6%; Pred. No. 1.1e-189;
Matches 661; Conservative 0; Mismatches 17; Indels 6; Gaps 1;

QY 1 ATGAGAACATCCATCAGAGCTCTAGGACCCCTGCTCGTGTACAGCGGGGTTTTC 60
DB 1 ATGAGAACACCATCAGAGCTCTAGGACCCCTGCTCGTGTACAGCGGGGTTTTC 60

QY 61 TTCTTCACAAATCTCTCAATACCGCAGCTAGACTCGTGTGGACTTCTCTCAAT 120
DB 61 TTCTTCACAAATCTCTCAATACCGCAGCTAGACTCGTGTGGACTTCTCTCAAT 120

QY 121 TTCTTAGGGGAACACCCGCTGTCTTGGCCAAATTCGACGTCCTCCAGTCAAC 180
DB 121 TTCTTAGGGGAACACCCGCTGTCTTGGCCAAATTCGACGTCCTCCAGTCAAC 180

QY 181 TCACCAACCTGTGTCTCTCAATTTGCTGTGTATCGTGTATCGTGTGGGCTTTT 240
DB 181 TCACCAACCTGTGTCTCTCAATTTGCTGTGTATCGTGTATCGTGTGGGCTTTT 240

QY 241 ATCATCTTCTCTGCACTCGTGTATCGTGTATCGTGTATCGTGTATCGTGTAT 300
DB 241 ATCATCTTCTCTGCACTCGTGTATCGTGTATCGTGTATCGTGTATCGTGTAT 300

QY 301 CAAGGTATGTGGCGGTTTGTCTCTAAATTCAGGATCAACAAACAGCAGCGGACCA 360
DB 301 CAAGGTATGTGGCGGTTTGTCTCTAAATTCAGGATCAACAAACAGCAGCGGACCA 360

QY 361 TG-----CAAAACCTGCACACTCTGTCTCAGGAACTCTATGTTTCCCTCATGTCG 414
DB 361 TGAGGAACACAACTTCAGACTCTTGTCTCAAGGAACCTTATGTTTCCCTCATGTCG 420

QY 415 TGTACAAAACCTACGACAGAACTGCACCTGTATTCCTCATCCCATCATCTTGGGCTTTC 474

DB 421 TGTACAAAACCTACGACAGAACTGCACCTGTATTTCCCATCCATCATCTTGGGCTTTC 480
QY 475 GCAAAATACCTATGGAGTGGGCTCAGTCCGTTCTCTTGGCTCAGTTTACTAGTGCCA 534
DB 481 GCAAAATTCCTATGGAGTGGGCTCAGTCCGTTCTCTTGGCTCAGTTTACTAGTGCCA 540
QY 535 TTCTTTCAGTGGTTTCGTAGGGCTTTCCCCACCTGTCTGGGCTTTCAGTTATATGATGATG 594
DB 541 TTCTTTCAGTGGTTTCGTAGGGCTTTCCCCACCTGTCTGGGCTTTCAGTTATATGATGATG 600
QY 595 TGGTTTTGGGGGCCAAGTCTGTACAACTCTGAGTCCCTTTATGCGGCTGTACCAATT 654
DB 601 TGGTATTGGGGGCCAAGTCTGTACAACTCTGAGTCCCTTTATGCGGCTGTACCAATT 660
QY 655 TTCTTTTGTCTTTTGGGTATACATT 678
DB 661 TTCTATTGTCTTTTGGGTATACATT 684

RESULT 7
US-08-059-031-1
Sequence 1, Application US/08059031
Patent No. 5595739
GENERAL INFORMATION:
APPLICANT: CARMAN, WILLIAM
APPLICANT: DECKER, RICHARD H
APPLICANT: WALLACE, LESLEY
APPLICANT: MIMMS, LARRY T
APPLICANT: SOLOMON, LARRY R
TITLE OF INVENTION: HEPATITIS B VIRUS MUTANTS, REAGENTS AND METHODS FOR DETECTION
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: ABBOTT LABORATORIES D377/AP6D
STREET: ONE ABBOTT PARK ROAD
CITY: ABBOTT PARK
STATE: IL
COUNTRY: USA
ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/059,031
FILING DATE:
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: FOREMSKI, PRISCILLA E.
REGISTRATION NUMBER: 33,207
REFERENCE/DOCKET NUMBER: 5347.US.01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 708-937-6365
TELEFAX: 708-938-2623
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 684 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 1..684
US-08-059-031-1

Query Match 93.2%; Score 634.8; DB 1; Length 684;
Best Local Similarity 96.6%; Pred. No. 1.1e-189;
Matches 661; Conservative 0; Mismatches 17; Indels 6; Gaps 1;

QY 1 ATGAGAACATCCATCAGAGCTCTAGGACCCCTGCTCGTGTACAGCGGGGTTTTC 60
DB 1 ATGAGAACACCATCAGAGCTCTAGGACCCCTGCTCGTGTACAGCGGGGTTTTC 60

RESULT 9
PCT-US94-05090-1
; Sequence 1, Application PC/TUS9405090
; GENERAL INFORMATION:
; APPLICANT: CARMAN, WILLIAM
; APPLICANT: DECKER, RICHARD H
; APPLICANT: WALLACE, LESLEY
; APPLICANT: MIMMS, LARRY T
; APPLICANT: SOLOMON, LARRY R
; TITLE OF INVENTION: HEPATITIS B VIRUS MUTANTS, REAGENTS AND METHODS FOR DETECTION
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ABBOTT LABORATORIES D377/AP6D
; STREET: ONE ABBOTT PARK ROAD
; CITY: ABBOTT PARK
; STATE: IL
; COUNTRY: USA
; ZIP: 60064-3500
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/05090
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: POREMSKI, PRISCILLA E.
; REGISTRATION NUMBER: 33,207
; REFERENCE/DOCKET NUMBER: 5347.US.01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 708-937-6365
; TELEFAX: 708-938-2623
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 684 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..684
PCT-US94-05090-1

Query Match 93.2%; Score 634.8; DB 5; Length 684;
Best Local Similarity 96.6%; Pred. NO. 1.1e-189;
Matches 661; Conservative 0; Mismatches 17; Indels 6; Gaps 1;
QY 1 ATGGAGACATCGCATCAGGACTCCTAGGACCCCTGCTGCTAGACCTCGTGTGAGCTTCTCTCAAT 60
DB 1 ATGGAGACACCAATCCTCAATACCAATACCAATACCAATACCAATACCAATACCAATACCAAT 60
QY 61 TTGTTGACAAAATCCTCAATACCAATACCAATACCAATACCAATACCAATACCAATACCAAT 120
DB 61 TTGTTGACAAAATCCTCAATACCAATACCAATACCAATACCAATACCAATACCAATACCAAT 120
QY 121 TTTCTAGGGGGAACACCGGTGTCTTGGCCAAAATTCGAGTCCCAATCTCCAGTAC 180
DB 121 TTTCTAGGGGGAACACCGGTGTCTTGGCCAAAATTCGAGTCCCAATCTCCAGTAC 180
QY 181 TCACCAACCTGTGTCTCTCAATTTGTCCTGTTATCGTGGATGTGTCTGGCGGTTT 240
DB 181 TCACCAACCTGTGTCTCTCAATTTGTCCTGTTATCGTGGATGTGTCTGGCGGTTT 240
QY 241 ATCATCTTCTCTGCAATCTGCTGCTATGCTCAATCTTCTGTTGTTTCTTCTGACTAT 300
DB 241 ATCATCTTCTCTGCAATCTGCTGCTATGCTCAATCTTCTGTTGTTTCTTCTGACTAT 300
QY 301 CAAGGTATGTTGGCGGTTTGTCTCTCAATTTCCAGGATCAACACACACCGACCGACCA 360
DB 301 CAAGGTATGTTGGCGGTTTGTCTCTCAATTTCCAGGATCAACACACACCGACCGACCA 360

QY 361 TG-----CAAAACCTGCACAACTCCTGCTCAAGGAACCTCTATGTTTCCCTCATGTTGC 414
DB 361 TGCAGGAACACAACTGCACGACTCCTGCTCAAGGAACCTCTATGTTTCCCTCATGTTGC 420
QY 415 TGTACAAAACCTACGGACAGAACTGCACCTGTTATCCCATCCCATCATCTTGGGCTTTC 474
DB 421 TGTACAAAACCTACGGACAGAACTGCACCTGTTATCCCATCCCATCATCTTGGGCTTTC 480
QY 475 GCAAAATACCTATCGGAGTGGGCTCAGTCCGTTTCTTCTGCTCAGTCTTACTAGTGCCA 534
DB 481 GCAAAATTCCTAUGGAGTGGGCTCAGTCCGTTTCTTCTGCTCAGTCTTACTAGTGCCA 540
QY 535 TTTCTTTCAGTGGTTCGTAGGGCTTTCCCACTGCTGCTGGCTTTCAGTTATATGATGATG 594
DB 541 TTTCTTTCAGTGGTTCGTAGGGCTTTCCCACTGCTGCTGGCTTTCAGTTATATGATGATG 600
QY 595 TGGTTTGGGGGCGCAAGTCTGTACAACTCTTGGATCCCTTTATGCGGCTGTTACCAATT 654
DB 601 TGGTATTGGGGGCGCAAGTCTGTACAACTCTTGGATCCCTTTATGCGGCTGTTACCAATT 660
QY 655 TTCTTTTGTCTTTCGGTATACATT 678
DB 661 TTCTATTGTCTTTCGGTATACATT 684
RESULT 10
US-08-500-914A-1
; Sequence 1, Application US/08500914A
; Patent No. 5856084
; GENERAL INFORMATION:
; APPLICANT: KARAYIANIS, PETER
; APPLICANT: THOMAS, HOWARD C.
; TITLE OF INVENTION: HEPATITIS B VACCINE
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHUYE P.C.
; STREET: 1100 NORTH GLEBE ROAD, 8TH FLOOR
; CITY: ARLINGTON
; STATE: VIRGINIA
; COUNTRY: U.S.A.
; ZIP: 22201-4714
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/500,914A
; FILING DATE: 28-DEC-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: MITCHARD, LEONARD C.
; REGISTRATION NUMBER: 29,009
; REFERENCE/DOCKET NUMBER: 1208-17
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-816-4000
; TELEFAX: 703-816-4100
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 893 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-500-914A-1
Query Match 92.7%; Score 631.4; DB 2; Length 893;
Best Local Similarity 95.4%; Pred. NO. 1.5e-188;
Matches 650; Conservative 0; Mismatches 31; Indels 0; Gaps 0;
QY 1 ATGGAGACATCGCATCAGGACTCCTAGGACCCCTGCTGCTGTTTACAGCGGGGTTTTC 60

Db 129 ATGAGAACATCATCAGGATTCCTAGGACCCCTGCTGTGTTACAGGGGGTTTTTC 188
Qy 61 TTGTTGACAAATTCCTCAATACCGCAGAGTCTAGACTCGTGGTGGACTTCTCTCAAT 120
Db 189 TTGTTGACAAATTCCTCAATACCGCAGAGTCTAGACTCGTGGTGGACTTCTCTCAAT 248
Qy 121 TTCTAGGGGGAACACCGGTGTCTTGGCCAAATTCGAGTCCCAATCTCCAGTCA 180
Db 249 TTCTAGGGGGAATCTCCGGTGTCTTGGCCAAATTCGAGTCCCAATCTCCAGTCA 308
Qy 181 TCACCAACCTGTTGCTCTCAATTTGCTGTGTTATCGCTGGATGTCTGCGGGTTTTT 240
Db 309 TCACCAACCTGCTGCTCTCAATTTGCTGTGTTATCGCTGGATGTCTGCGGGTTTTT 368
Qy 241 ATCATCTTCTCTGCTATGCTGCTATGCTCTCTCTCTCTCTCTCTCTCTCTCTCT 300
Db 369 ATCATATCT 428
Qy 301 CAAGGTATGTTGCGCGTTTGTCTCTAAATTCAGGATCAACAAACACGACCGGACCA 360
Db 429 CAAGGTATGTTGCGCGTTTGTCTCTAAATTCAGGATCAACAAACACGACCGGACCA 488
Qy 361 TGCACCAACCTGCACTCTGCTCAAGGAACTCTATGTTTCCCTCATGTTGCTGTACA 420
Db 489 TGCACCAACCTGCACTCTGCTCAAGGAACTCTATGTTTCCCTCATGTTGCTGTACA 548
Qy 421 AAACCTACGACAGAACTGCACTGATTTCCATCCATCCATCTTGGGCTTTCGCAAAA 480
Db 549 AAACCTACGAGTGAATGCACTGATTTCCATCCATCCATCTTGGGCTTTCGCAAAA 608
Qy 481 TACCTATGGAGTGGGCTCAGTCCGTTCTCTTGGCTCAGTTTACTAGTGCATTTGTT 540
Db 609 TACCTATGGAGTGGGCTCAGTCCGTTCTCTTGGCTCAGTTTACTAGTGCATTTGTT 668
Qy 541 CAGTGGTTCGTAGGGTTTCCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 600
Db 669 CAGTGGTTCGTAGGGTTTCCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 728
Qy 601 TGGGGGCCAAGTCTGTACAACTCTGAGTCCCTTTATGCGCTGTTACCAATTTCTTT 660
Db 729 TGGGGGCCAAGTCTGTACAACTCTGAGTCCCTTTATGCGCTGTTACCAATTTCTTT 788
Qy 661 TGCTTTGGGTATACATTTAA 681
Db 789 TGCTCTGGGTATACATTTAA 909

RESULT 11

5196194-15
; Patent No. 5196194
; APPLICANT: RUTTER, WILLIAM J.; GOODMAN, HOWARD M.
; TITLE OF INVENTION: VACCINES CONTAINING HEPATITIS B S-PROTEIN
; NUMBER OF SEQUENCES: 21
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/679,621
; FILING DATE: 7-DEC-1984
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 513,055
; FILING DATE: 12-JUL-1983
; APPLICATION NUMBER: 107,267
; FILING DATE: 21-DEC-1979
; APPLICATION NUMBER: 41,909
; FILING DATE: 24-MAY-1979
; SEQ ID NO:15:
; LENGTH: 3220
5196194-15
Query Match 92.7%; Score 631.4; DB 6; Length 3220;
Best Local Similarity 95.4%; Pred. No. 3e-188;
Matches 650; Conservative 0; Mismatches 31; Indels 0; Gaps 0;

Db 1564 ATGAGAACATCATCAGGATTCCTAGGACCCCTGCTGTGTTACAGGGGGTTTTTC 1623
Qy 61 TTGTTGACAAATTCCTCAATACCGCAGAGTCTAGACTCGTGGTGGACTTCTCTCAAT 120
Db 1624 TTGTTGACAAATTCCTCAATACCGCAGAGTCTAGACTCGTGGTGGACTTCTCTCAAT 1683
Qy 121 TTCTAGGGGGAACACCGGTGTCTTGGCCAAATTCGAGTCCCAATCTCCAGTCA 180
Db 1684 TTCTAGGGGGAATCTCCGGTGTCTTGGCCAAATTCGAGTCCCAATCTCCAGTCA 1743
Qy 181 TCACCAACCTGTTGCTCTCAATTTGCTGTGTTATCGCTGGATGTCTGCGGGTTTTT 240
Db 1744 TCACCAACCTGCTGCTCTCAATTTGCTGTGTTATCGCTGGATGTCTGCGGGTTTTT 1803
Qy 241 ATCATCTTCTCTGCTATGCTGCTATGCTCTCTCTCTCTCTCTCTCTCTCTCTCT 300
Db 1804 ATCATATCT 1863
Qy 301 CAAGGTATGTTGCGCGTTTGTCTCTAAATTCAGGATCAACAAACACGACCGGACCA 360
Db 1864 CAAGGTATGTTGCGCGTTTGTCTCTAAATTCAGGATCAACAAACACGACCGGACCA 1923
Qy 361 TGCACCAACCTGCACTCTGCTCAAGGAACTCTATGTTTCCCTCATGTTGCTGTACA 420
Db 1924 TGCACCAACCTGCACTCTGCTCAAGGAACTCTATGTTTCCCTCATGTTGCTGTACA 1983
Qy 421 AAACCTACGACAGAACTGCACTGATTTCCATCCATCCATCTTGGGCTTTCGCAAAA 480
Db 1984 AAACCTACGAGTGAATGCACTGATTTCCATCCATCCATCTTGGGCTTTCGCAAAA 2043
Qy 481 TACCTATGGAGTGGGCTCAGTCCGTTCTCTTGGCTCAGTTTACTAGTGCATTTGTT 540
Db 2044 TACCTATGGAGTGGGCTCAGTCCGTTCTCTTGGCTCAGTTTACTAGTGCATTTGTT 2103
Qy 541 CAGTGGTTCGTAGGGTTTCCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 600
Db 2104 CAGTGGTTCGTAGGGTTTCCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2163
Qy 601 TGGGGGCCAAGTCTGTACAACTCTGAGTCCCTTTATGCGCTGTTACCAATTTCTTT 660
Db 2164 TGGGGGCCAAGTCTGTACAACTCTGAGTCCCTTTATGCGCTGTTACCAATTTCTTT 2223
Qy 661 TGCTTTGGGTATACATTTAA 681
Db 2224 TGCTCTGGGTATACATTTAA 2244

RESULT 12

US-08-715-808-1
; Sequence 1, Application US/08715808
; Patent No. 5981274
; GENERAL INFORMATION:
; APPLICANT: Tyrrell, D. Lorne J.
; APPLICANT: Chaisomchit, Sumonta
; APPLICANT: Chang, Lung-Ji
; TITLE OF INVENTION: Recombinant Hepatitis Virus Vectors
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Medlen & Carroll, LLP
; STREET: 220 Montgomery Street, Suite 2200
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/715,808
; FILING DATE: 18-SEP-1996

Qy 1 ATGAGAACATCATCAGGATTCCTAGGACCCCTGCTGTGTTACAGGGGGTTTTTC 60

ATTORNEY/AGENT INFORMATION:
NAME: Ingolia, Diane E.
REGISTRATION NUMBER: 40,027
REFERENCE/DOCKET NUMBER: CHANG-02441
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 705-8410
TELEFAX: (415) 397-8338
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 3221 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "DNA"
US-08-715-808-1

Query Match 92.7%; Score 631.4; DB 2; Length 3221;
Best Local Similarity 95.4%; Pred. No. 3e-188;
Matches 650; Conservative 0; Mismatches 31; Indels 0; Gaps 0;

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QY 1 ATGGAGAACATCGCATCAGGACTCCTAGGACCCCTGCTGGTGTACAGCGGGGTTTTTC 60
Db 157 ATGGAGAACATCAGATCAGGATTCCTAGGACCCCTGCTGGTGTACAGCGGGGTTTTTC 216

QY 61 TTGTTGACAAAAATCCTCAATACCGCAGAGTCTAGACTCGTGGTGGACTTCTCTCAAT 120
Db 217 TTGTTGACAGAATCCTCAATACCGCAGAGTCTAGACTCGTGGTGGACTTCTCTCAAT 276

QY 121 TTCTAGGGGGAACACCGGTGCTCTTGGCCAAATTCGCAGTCCCAATCTCCAGTCA 180
Db 277 TTCTAGGGGGAATCTCCCGGTGCTCTTGGCCAAATTCGCAGTCCCAATCTCCAGTCA 336

QY 181 TCACCAACCTGTTGCTCTCCAAATTTGCTGTTATCGCTGGATGTCTGCGGGGTTTT 240
Db 337 TCACCAACCTGTTGCTCTCCAAATTTGCTGTTATCGCTGGATGTCTGCGGGGTTTT 396

QY 241 ATCATCTTCTTGATCTCTGCTGCTATGCTCATCTTCTGTTGTTCTTCTGGAATAT 300
Db 397 ATCATATCTCTTCTGCTGCTGCTATGCTCATCTTCTGTTGTTCTTCTGGAATAT 456

QY 301 CAAGGTATGTTGCCGTTTCTCTCTAAATTCAGGATCAACAACACCGACCGGACCA 360
Db 457 CAAGGTATGTTGCCGTTTCTCTCTAAATTCAGGATCAACAACACCGACCGGACCA 516

QY 361 TGCACAACTGCAACATCTCTGCTCAAGGAACCTCTATGTTTCCCTCATGTTGCTGTACA 420
Db 517 TGCACAACTGCAACATCTCTGCTCAAGGAACCTCTATGTTTCCCTCATGTTGCTGTACA 576

QY 421 AAACCTACGACAGAACTGCATCTGTTATTCCTATCCCATCCCATCTTGGGTTTTCGCAAAA 480
Db 577 AAACCTACGACAGAACTGCATCTGTTATTCCTATCCCATCCCATCTTGGGTTTTCGCAAAA 636

QY 481 TACCTATGGAGTGGGCTCAGTCCGTTTCTCTTGGCTCAGTTTACTAGTGGCAATTTGTT 540
Db 637 TACCTATGGAGTGGGCTCAGTCCGTTTCTCTTGGCTCAGTTTACTAGTGGCAATTTGTT 696

QY 541 CAGTGGTTCTGAGGCTTTCCTCCCATGCTGCTGGCTTTCAGTTATATGATGATGTTT 600
Db 697 CAGTGGTTCTGAGGCTTTCCTCCCATGCTGCTGGCTTTCAGTTATATGATGATGTTT 756

QY 601 TGGGGGCAAGCTCTGTACAACTCTTGAGTCCCTTTATGCGGCTGTATACCAATTTCTTT 660
Db 757 TGGGGGCAAGCTCTGTACAACTCTTGAGTCCCTTTATGCGGCTGTATACCAATTTCTTT 816

QY 661 TGTCTTTGGGTATACATTTAA 681
Db 817 TGTCTTTGGGTATACATTTAA 837
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RESULT 13
US-08-760-797A-2
; Sequence 2, Application US/08760797A

Patent No. 5928902
GENERAL INFORMATION:
APPLICANT: De Wilde, Michel
APPLICANT: Cohen, Joseph
TITLE OF INVENTION: Hybrid Protein Between CS
TITLE OF INVENTION: from Plasmodium and HBSAG
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
CITY: King of Prussia
STATE: PA
COUNTRY: USA
ZIP: 19406
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/760,797A
FILING DATE: 04-DEC-1996
CLASSIFICATION: 435
PRIOR APPLICATION NUMBER: 08/442,612
FILING DATE: 17-MAY-1995
ATTORNEY/AGENT INFORMATION:
NAME: Baumeister, Kirk
REGISTRATION NUMBER: 33,833
REFERENCE/DOCKET NUMBER: B45015-1C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-5096
TELEFAX: 610-270-5090
TELEX:
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 3504 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-760-797A-2

Query Match 92.7%; Score 631.4; DB 2; Length 3504;
Best Local Similarity 95.4%; Pred. No. 3.1e-188;
Matches 650; Conservative 0; Mismatches 31; Indels 0; Gaps 0;

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QY 1 ATGGAGAACATCGCATCAGGACTCCTAGGACCCCTGCTGGTGTACAGCGGGGTTTTTC 60
Db 1653 ATGGAGAACATCAGATCAGGATTCCTAGGACCCCTGCTGGTGTACAGCGGGGTTTTTC 1712

QY 61 TTGTTGACAAAAATCCTCAATACCGCAGAGTCTAGACTCGTGGTGGACTTCTCTCAAT 120
Db 1713 TTGTTGACAGAATCCTCAATACCGCAGAGTCTAGACTCGTGGTGGACTTCTCTCAAT 1772

QY 121 TTCTAGGGGGAACACCGGTGCTCTTGGCCAAATTCGCAGTCCCAATCTCCAGTCA 180
Db 1773 TTCTAGGGGGAATCAGCGGTGCTCTTGGCCAAATTCGCAGTCCCAATCTCCAGTCA 1832

QY 181 TCACCAACCTGTTGCTCTCCAAATTTGCTGTTATCGCTGGATGTCTGCGGGGTTTT 240
Db 1833 TCACCAACCTGTTGCTCTCCAAATTTGCTGTTATCGCTGGATGTCTGCGGGGTTTT 1892

QY 241 ATCATCTTCTCTGCTGCTGCTATGCTCATCTTCTTGTGTTCTTCTGGAATAT 300
Db 1893 ATCATATCTCTCTGCTGCTGCTATGCTCATCTTCTTGTGTTCTTCTGGAATAT 1952

QY 301 CAAGGTATGTTGCCGTTTCTCTCTAAATTCAGGATCAACAACACCGACCGGACCA 360
Db 1953 CAAGGTATGTTGCCGTTTCTCTCTAAATTCAGGATCAACAACACCGGACCA 2012

QY 361 TGCACAACTGCAACATCTCTGCTCAAGGAACCTCTATGTTTCCCTCATGTTGCTGTACA 420
Db 2013 TGCACAACTGCAACATCTCTGCTCAAGGAACCTCTATGTTTCCCTCATGTTGCTGTACA 2072
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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/760,797
; FILING DATE: 04-DEC-1996
; APPLICATION NUMBER: 08/442,612
; FILING DATE: 17-MAY-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Baumeister, Kirk
; REGISTRATION NUMBER: 33,833
; REFERENCE/DOCKET NUMBER: B45015-1FWC2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-270-5096
; TELEFAX: 610-270-5090
; TELEX:
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3504 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
;
US-08-932-929B-2

Query Match 92.7%; Score 631.4; DB 3; Length 3504;
Best Local Similarity 95.4%; Pred. No. 3.1e-188;
Matches 650; Conservative 0; Mismatches 31; Indels 0; Gaps 0;
QY 1 ATGGAGAACATCGCATCAGACTCCTAGACCCCTGCTGTTACAGGGGGGTTTTC 60
Db 1653 ATGGAGAACATCATCAGGATTCCTAGGACCCCTGCTGTTACAGGGGGGTTTTC 1712
QY 61 TTGTTGACAAAAATCCTCACAATACCGCAGAGCTAGACTCGTGTGGACTTCTCTCAAT 120
Db 1713 TTGTTGACAGATCCTCACAATACCGCAGAGCTAGACTCGTGTGGACTTCTCTCAAT 1772
QY 121 TTTCTAGGGGGAAACACCCGTGTCTTGGCCAAAATTCGAGTCCCAATCTCCAGTCA 180
Db 1773 TTTCTAGGGGGATCACCCGTGTCTTGGCCAAAATTCGAGTCCCAATCTCCATCAC 1832
QY 181 TCACCAACCTGTGTCCTCAATTTGTCGGTTATCGCTGGATGTCTGGGGCGTTTT 240
Db 1833 TCACCAACCTTCTGTCCTCAATTTGTCGGTTATCGCTGGATGTCTGGGGCGTTTT 1892
QY 241 ATCATCTTCTCTGCACTCTGCTGCTATGCTCATCTTCTTGTGGTTCTTCTGGACTAT 300
Db 1893 ATCATATTCTCTTCACTCTGCTGCTATGCTCATCTTCTTATTGGTTCTTCTGGATTAT 1952
QY 301 CAAGGTATGTGGCGTTTGTCTCTAATTCAGGATCAACAACACCGACCGGACCA 360
Db 1953 CAAGGTATGTGGCGTTTGTCTCTAATTCAGGATCAACAACACCGATACGGACCA 2012
QY 361 TGCAAAACCTGCACAACTCCTGCTCAAGGAACCTCTATGTTCCCTCATGTTGCTGTACA 420
Db 2013 TGCAAAACCTGCACGACTCTCTGCTCAAGGCACTCTATGTTTCCCTCATGTTGCTGTACA 2072
QY 421 AAACCTACGGACAGAAACTGCACTGATTCCTATCCCATCCCATCTTGGGCTTTCGCAAAA 480
Db 2073 AAACCTACGGATGGAATTCGACTGATTCCTATCCCATCCCATCTTGGGCTTTCGCAAAA 2132
QY 481 TACCTATGGGAGTGGGCTCAGTCCGTTTCTTGGCTCAGTTTACTAGTGCCATTGTT 540
Db 2133 TACCTATGGGAGTGGGCTCAGTCCGTTTCTTGGCTCAGTTTACTAGTGCCATTGTT 2192
QY 541 CAGTGGTTCGTAGGGCTTTCCGCCACTGTCTGGCTTTCAGTTATATGATGATGTGTT 600
Db 2193 CAGTGGTTCGTAGGGCTTTCCGCCACTGTCTGGCTTTCAGTTATATGATGATGTGTTAT 2252
QY 601 TGGGGGCCAGTCTGTACACATCTGAGTCCCTTATGCGCTGTATACCAATTTCTTT 660
Db 2253 TGGGGGCCAAGTCTGTACAGATCTGAGTCCCTTATACCGCTGTATACCAATTTCTTT 2312
QY 661 TGCTTTGGGTATACATTTAA 681
Db 2313 TGCTCTGGGTATACATTTAA 2333

Search completed: July 26, 2004, 15:26:48
Job time : 81 secs

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OM nucleic - nucleic search, using sw model

Run on: July 26, 2004, 14:45:15 ; Search time 410 Seconds
(without alignments)
8119.346 Million cell updates/sec

Title: US-09-719-533A-1_COPY_155_835

Perfect score: 681
Sequence: 1 ATGGAGACATCGCATCAGG.....GTCTTGGGTACATTAA 681

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 3216467 seqs, 2444149694 residues

Total number of hits satisfying chosen parameters: 6432934

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA:*

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2: /cgn2_6/prodata/1/pubpna/PCT_NEW_PUB.seq:
3: /cgn2_6/prodata/1/pubpna/US06_NEW_PUB.seq:
4: /cgn2_6/prodata/1/pubpna/US06_PUBCOMB.seq:
5: /cgn2_6/prodata/1/pubpna/US07_NEW_PUB.seq:
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7: /cgn2_6/prodata/1/pubpna/US08_NEW_PUB.seq:
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11: /cgn2_6/prodata/1/pubpna/US09C_PUBCOMB.seq:
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15: /cgn2_6/prodata/1/pubpna/US10C_PUBCOMB.seq:
16: /cgn2_6/prodata/1/pubpna/US10D_PUBCOMB.seq:
17: /cgn2_6/prodata/1/pubpna/US10_NEW_PUB.seq:
18: /cgn2_6/prodata/1/pubpna/US60_NEW_PUB.seq:
19: /cgn2_6/prodata/1/pubpna/US60_PUBCOMB.seq:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	673	98.8	3215	13	US-10-453-792-287
2	669.8	98.4	3215	13	US-10-453-792-285
3	666.6	97.9	3215	13	US-10-453-792-286
4	663.4	97.4	3215	13	US-10-453-792-283
5	639.4	93.9	3221	13	US-10-453-792-283
6	632.6	92.9	1365	16	US-10-365-620-33
7	632.6	92.9	2037	16	US-10-365-620-28
8	632.6	92.9	2037	16	US-10-365-620-31
9	631.4	92.7	1696	15	US-10-267-922-15
10	631.4	92.7	3200	13	US-10-453-792-280
11	631.4	92.7	3221	13	US-10-453-792-279
12	631.4	92.7	4084	10	US-09-781-891D-21
13	631.4	92.7	4496	10	US-09-781-891D-22
14	629.8	92.5	3182	13	US-10-453-792-304

Sequence 3, Appli
Sequence 7, Appli
Sequence 133, App
Sequence 133, App
Sequence 133, App
Sequence 310, App
Sequence 281, App
Sequence 303, App
Sequence 307, App
Sequence 6, Appli
Sequence 1, Appli
Sequence 302, App
Sequence 299, App
Sequence 11, Appl
Sequence 301, App
Sequence 14, Appl
Sequence 14, Appl
Sequence 14, Appl
Sequence 309, App
Sequence 1, Appli
Sequence 3, Appli
Sequence 4, Appli
Sequence 282, App
Sequence 15, Appl
Sequence 15, Appl
Sequence 15, Appl
Sequence 15, Appl
Sequence 308, App
Sequence 13, Appli
Sequence 1, Appli

ALIGNMENTS

RESULT 1

US-10-453-792-287

; Sequence 287, Application US/10453792

; Publication No. US20040029110A1

; GENERAL INFORMATION:

; APPLICANT: STUYVER, LIEVEN

; ROSSAU, RUDI

; MAERTENS, GEERT

; TITLE OF INVENTION: METHOD FOR TYPING AND DETECTING HBV

; NUMBER OF SEQUENCES: 313

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: NIXON & VANDERHVE P.C.

; STREET: 1100 NORTH GLEBE ROAD

; CITY: ARLINGTON

; STATE: VIRGINIA

; COUNTRY: U.S.A.

; ZIP: 22201-4714

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/10/453,792

; FILING DATE: 04-Jun-2003

; CLASSIFICATION: <Unknown>

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US/09/155,885A

; FILING DATE: 08-Oct-1998

; APPLICATION NUMBER: PCT/EP97/02002

; FILING DATE: 21-APR-1997

; APPLICATION NUMBER: EP 96870053.4

; FILING DATE: 19-APR-1996

; ATTORNEY/AGENT INFORMATION:

; NAME: SADOFF, B.J.

; REGISTRATION NUMBER: 36,663

; REFERENCE/DOCKET NUMBER: 2551-5

TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 816-4000
TELEFAX: (703) 816-4100
INFORMATION FOR SEQ ID NO: 287:
SEQUENCE CHARACTERISTICS:
LENGTH: 3215 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOHETICAL: NO
ANTI-SENSE: NO
SEQUENCE DESCRIPTION: SEQ ID NO: 287:
US-10-453-792-287

Query Match 98.4%; Score 669.8; DB 13; Length 3215;
Best Local Similarity 99.3%; Pred. No. 2.7e-209;
Matches 676; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 ATGAGAACATCGCATCAGGACTCCTAGGACCCCTGCTCGTGTATACAGCGGGTTTTTC 60
Db 157 ATGAGAACATCGCATCAGGACTCCTAGGACCCCTGCTCGTGTATACAGCGGGTTTTTC 216

Qy 61 TTGTTGACAAAATCCTCAATACCGCAGAGCTAGCTCGGTGGGACTTCTCTCAAT 120
Db 217 TTGTTGACAAAATCCTCAATACCGCAGAGCTAGCTCGGTGGGACTTCTCTCAAT 276

Qy 121 TTTCTAGGGGAAACACCGGTGTGTCTTGGCCAAAATTCGCGATCCCAATCTCCAGTCA 180
Db 277 TTTCTAGGGGAAACACCGGTGTGTCTTGGCCAAAATTCGCGATCCCAATCTCCAGTCA 336

Qy 181 TCACCAACCTGTCTCTCAATTTGTCTGGTTATCGCTGGATGTCTCGCGCGTTTT 240
Db 337 TCACCAACCTGTCTCTCAATTTGTCTGGTTATCGCTGGATGTCTCGCGCGTTTT 396

Qy 241 ATCATCTCTCTGATCCTGCTGATGCTATCTCTTCTGTTTCTTCTGGACTAT 300
Db 397 ATCATCTCTCTGATCCTGCTGATGCTATCTCTTCTGTTTCTTCTGGACTAT 456

Qy 301 CAAGTATGTTGCCCGTTTGTCTCTAATTCAGGATCAACAAACAGCAGCAGCA 360
Db 301 CAAGTATGTTGCCCGTTTGTCTCTAATTCAGGATCAACAAACAGCAGCAGCA 360

Qy 361 TGAACAACTGCAACTCTGCTCAAGAACTCTATGTTCCCTCATGTTGCTGTACA 420
Db 517 TGAACAACTGCAACTCTGCTCAAGAACTCTATGTTCCCTCATGTTGCTGTACA 576

Qy 421 AAACCTACGAGCAAACTGCACTGATATCCCATCCCATCATCTTGGGCTTTCGAAA 480
Db 577 AAACCTACGAGCAAACTGCACTGATATCCCATCCCATCATCTTGGGCTTTCGAAA 636

Qy 481 TACCTATGGAGTGGGCTCAGTCCGTTCTCTTGGCTCAGTTTACTAGTGCATTTGT 540
Db 637 TACCTATGGAGTGGGCTCAGTCCGTTCTCTTGGCTCAGTTTACTAGTGCATTTGT 696

Qy 541 CAGTGGTTCGTAGGGCTTTCCCGCACTGCTGCGCTTTCAGTTATATGATGATGTT 600
Db 697 CAGTGGTTCGTAGGGCTTTCCCGCACTGCTGCGCTTTCAGTTATATGATGATGTT 756

Qy 601 TGGGGGCAAGTGTATACAACTTTGAGTCCCTTTATGCGCGTGTATCAATTTCTTT 660
Db 757 TGGGGGCAAGTGTATACAACTTTGAGTCCCTTTATGCGCGTGTATCAATTTCTTT 816

Qy 661 TGTCTTTGGGTATACATTTAA 681
Db 817 TGTCTTTGGGTATACATTTAA 837

RESULT 2

US-10-453-792-285
; Sequence 285, Application US/10453792
; Publication No. US20040029110A1
; GENERAL INFORMATION:

APPLICANT: STUYVER, LIEVEN
ROSSAU, RUDI
MAERTENS, GEERT
TITLE OF INVENTION: METHOD FOR TYPING AND DETECTING HBV
NUMBER OF SEQUENCES: 313
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERHUYE P.C.
STREET: 1100 NORTH GLEBE ROAD
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: U.S.A.
ZIP: 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/453,792
FILING DATE: 04-Jun-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/155,885A
FILING DATE: 08-Oct-1998
APPLICATION NUMBER: PCT/EP97/02002
FILING DATE: 21-Apr-1997
APPLICATION NUMBER: EP 96870053.4
FILING DATE: 19-Apr-1996
ATTORNEY/AGENT INFORMATION:
NAME: SADOFF, B.J.
REGISTRATION NUMBER: 36,663
REFERENCE/DOCKET NUMBER: 2551-5
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 816-4000
TELEFAX: (703) 816-4100
INFORMATION FOR SEQ ID NO: 285:
SEQUENCE CHARACTERISTICS:
LENGTH: 3215 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOHETICAL: NO
ANTI-SENSE: NO
SEQUENCE DESCRIPTION: SEQ ID NO: 285:
US-10-453-792-285

Query Match 98.4%; Score 669.8; DB 13; Length 3215;
Best Local Similarity 99.0%; Pred. No. 3.1e-208;
Matches 674; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 1 ATGAGAACATCGCATCAGGACTCCTAGGACCCCTGCTCGTGTATACAGCGGGTTTTTC 60
Db 157 ATGAGAACATCGCATCAGGACTCCTAGGACCCCTGCTCGTGTATACAGCGGGTTTTTC 216

Qy 61 TTGTTGACAAAATCCTCAATACCGCAGAGCTAGACTCGTGGTGGACTTCTCTCAAT 120
Db 217 TTGTTGACAAAATCCTCAATACCGCAGAGCTAGACTCGTGGTGGACTTCTCTCAAT 276

Qy 121 TTTCTAGGGGAAACACCGGTGTGTCTTGGCCAAAATTCGCGATCCCAATCTCCAGTCA 180
Db 277 TTTCTAGGGGAAACACCGGTGTGTCTTGGCCAAAATTCGCGATCCCAATCTCCAGTCA 336

Qy 181 TCACCAACCTGTCTCTCAATTTGTCTGGTTATCGCTGGATGTCTCGCGCGTTTT 240
Db 337 TCACCAACCTGTCTCTCAATTTGTCTGGTTATCGCTGGATGTCTCGCGCGTTTT 396

Qy 241 ATCATCTCTCTGATCCTGCTGATGCTATCTCTTCTGTTTCTTCTGGACTAT 300
Db 397 ATCATCTCTCTGATCCTGCTGATGCTATCTCTTCTGTTTCTTCTGGACTAT 456

Qy 301 CAAGTATGTTGCCCGTTTGTCTCTAATTCAGGATCAACAAACAGCAGCAGCA 360
Db 301 CAAGTATGTTGCCCGTTTGTCTCTAATTCAGGATCAACAAACAGCAGCAGCA 360

Db 457 CRAAGTATGTCGCCGTTGTCCTCTAATCCAGGATCATCAACACCGACCGACCA 516
QY 361 TGCAAACTCGCACACTCCTGCTCAAGGAACCTCTATGTTCCCTCATGTTGCTGTACA 420
Db 517 TGCAAACTCGCACACTCCTGCTCAAGGAACCTCTATGTTCCCTCATGTTGCTGTACA 576
QY 421 AAACCTACGACAGAACTGCACCTGTATCCCATCCCATCATCTTGGCTTCCGAAA 480
Db 577 AAACCTACGACAGAACTGCACCTGTATCCCATCCCATCATCTTGGCTTCCGAAA 636
QY 481 TACCTATGGAGTGGGCTTCAGTCCGTTTCTCTTGGCTCAGTTTACTAGTGCCATTGTT 540
Db 637 TACCTATGGAGTGGGCTTCAGTCCGTTTCTCTTGGCTCAGTTTACTAGTGCCATTGTT 696
QY 541 CAGTGTTCGTAGGCTTTCCTCCCACTGCTGCTTTCAGTTTACTAGTGATGATGTTT 600
Db 697 CAGTGTTCGTAGGCTTTCCTCCCACTGCTGCTTTCAGTTTACTAGTGATGATGTTT 756
QY 601 TGGGGCCCAAGTCTGTACAACTCTTGGCTTTCAGTCCGTTTACTAGTGATGATGTTT 660
Db 757 TGGGGCCCAAGTCTGTACAACTCTTGGCTTTCAGTCCGTTTACTAGTGATGATGTTT 816
QY 661 TGTCTTTGGGTATACATTAA 681
Db 817 TGTCTTTGGGTATACATTAA 837

RESULT 3
US-10-453-792-286
; Sequence 286, Application US/10453792
; Publication No. US20040029110A1
; GENERAL INFORMATION:
; APPLICANT: STUYVER, LIEVEN
; ROSSAU, RUDI
; MAERTENS, GEERT
; TITLE OF INVENTION: METHOD FOR TYPING AND DETECTING HBV
; NUMBER OF SEQUENCES: 313
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHVE P.C.
; STREET: 1100 NORTH GLEBE ROAD
; CITY: ARLINGTON
; STATE: VIRGINIA
; COUNTRY: U.S.A.
; ZIP: 22201-4714
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/453,792
; FILING DATE: 04-Jun-2003
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/155,885A
; FILING DATE: 08-Oct-1998
; APPLICATION NUMBER: PCT/EP97/02002
; FILING DATE: 21-Apr-1997
; APPLICATION NUMBER: EP 96870053.4
; FILING DATE: 19-Apr-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: SAOFF, B.J.
; REGISTRATION NUMBER: 36,663
; REFERENCE/DOCKET NUMBER: 2551-5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 816-4000
; TELEFAX: (703) 816-4100
; INFORMATION FOR SEQ ID NO: 286:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3215 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear

; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; SEQUENCE DESCRIPTION: SEQ ID NO: 286:
US-10-453-792-286
Query Match 97.9%; Score 666.6; DB 13; Length 3215;
Best Local Similarity 98.7%; Pred. No. 3.4e-207;
Matches 672; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
QY 1 ATGAGAGAACATCGCATCAGGACTCCTAGGACCCCTGCTGTTTACAGGGGGGTTTTC 60
Db 157 ATGAGAGAACATCGCATCAGGACTCCTAGGACCCCTGCTGTTTACAGGGGGGTTTTC 216
QY 61 TTGTTGACAAAATTCCTCAATACCCGACAGTCTAGACTCGTGTGAGACTTCTCTCAAT 120
Db 217 TTGTTGACAAAATTCCTCAATACCCGACAGTCTAGACTCGTGTGAGACTTCTCTCAAT 276
QY 121 TTCTAGGGGAAACACCGGTGTGCTTGGCCAAAATTCGAGTCCCAAAATTCACAGTCA 180
Db 277 TTCTAGGGGAAACACCGGTGTGCTTGGCCAAAATTCGAGTCCCAAAATTCACAGTCA 336
QY 181 TCACCAACCTGTTGCTCCTCAATTTGCTGCTGTTATCGCTGGATGTTCTGCGGCGTTT 240
Db 337 TCACCAACCTGTTGCTCCTCAATTTGCTGCTGTTATCGCTGGATGTTCTGCGGCGTTT 396
QY 241 ATCATCTTCTCTGCATCCTGCTGCTATGCTCATCTTCTTGTGTTTCTTCTGACTAT 300
Db 397 ATCATCTTCTCTGCATCCTGCTGCTATGCTCATCTTCTTGTGTTTCTTCTGACTAT 456
QY 301 CAAGGTATGTTGCCCGTTTGTCTTAATTCAGGATCAACAAACACAGCACCGGACCA 360
Db 457 CAAGGTATGTTGCCCGTTTGTCTTAATTCAGGATCAACAAACACAGCACCGGACCA 516
QY 361 TGGAAAACCTGCACAACTCCTGCTCAAGGACCTCTATGTTCCCTCATGTTGCTGTACA 420
Db 517 TGGAAAACCTGCACAACTCCTGCTCAAGGACCTCTATGTTCCCTCATGTTGCTGTACA 576
QY 421 AAACCTAGGACAGAACTGCACCTGTATTCCCATCCCATCATCTTGGGCTTTTCGAAAA 480
Db 577 AAACCTATGGATGGAACCTGCACCTGTATTCCCATCCCATCATCTTGGGCTTTTCGAAAA 636
QY 481 TACCTATGGAGTGGGCTCAGTCCGTTTCTCTTGGCTCAGTTTACTAGTGCCATTGTT 540
Db 637 TACCTATGGAGTGGGCTCAGTCCGTTTCTCTTGGCTCAGTTTACTAGTGCCATTGTT 696
QY 541 CAGTGTTCGTAGGCTTTTCCGCCACTGTCTGGCTTTTCAAGTTATATGATGATGTTT 600
Db 697 CAGTGTTCGTAGGCTTTTCCGCCACTGTCTGGCTTTTCAAGTTATATGATGATGTTT 756
QY 601 TGGGGGCAAGTCTGTACAACTTGGAGTCCCTTTATGCGCTGTTACCAATTTCTTT 660
Db 757 TGGGGGCAAGTCTGTACAACTTGGAGTCCCTTTATGCGCTGTTACCAATTTCTTT 816
QY 661 TGTCTTTGGGTATACATTAA 681
Db 817 TGTCTTTGGGTATACATTAA 837

RESULT 4
US-10-453-792-284
; Sequence 284, Application US/10453792
; Publication No. US20040029110A1
; GENERAL INFORMATION:
; APPLICANT: STUYVER, LIEVEN
; ROSSAU, RUDI
; MAERTENS, GEERT
; TITLE OF INVENTION: METHOD FOR TYPING AND DETECTING HBV
; NUMBER OF SEQUENCES: 313
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHVE P.C.
; STREET: 1100 NORTH GLEBE ROAD
; CITY: ARLINGTON

STATE: VIRGINIA
COUNTRY: U.S.A.
ZIP: 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/453,792
FILING DATE: 04-Jun-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/155,885A
FILING DATE: 08-Oct-1998
APPLICATION NUMBER: PCT/EP97/02002
FILING DATE: 21-Apr-1997
APPLICATION NUMBER: EP 96870053.4
FILING DATE: 19-Apr-1996
ATTORNEY/AGENT INFORMATION:
NAME: SADOFF, B.J.
REGISTRATION NUMBER: 36,663
REFERENCE/DOCKET NUMBER: 2551-5
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 816-4000
TELEFAX: (703) 816-4100
INFORMATION FOR SEQ ID NO: 283:
SEQUENCE CHARACTERISTICS:
LENGTH: 3221 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
SEQUENCE DESCRIPTION: SEQ ID NO: 283:
US-10-453-792-283

Query Match 97.4%; Score 663.4; DB 13; Length 3215;
Best Local Similarity 98.4%; Pred. No. 3.8e-206; Indels 0; Gaps 0;
Matches 670; Conservative 0; Mismatches 11;

QY 1 ATGAGAACATCGCATCAGGACTCTAGGACCCCTGCTGTTACAGCGGGGTTTTC 60
DB 157 ATGAGAACATCGCATCAGGACTCTAGGACCCCTGCTGTTACAGCGGGGTTTTC 216
QY 61 TTGTTGACAAATCTCACAATACCCAGAGTCTAGACTCGGTGGTACTTCTCAAT 120
DB 217 TCGTTGACAAATCTCACAATACCTCTAGACTCGGTGGTACTTCTCTCAAT 276
QY 121 TTCTTAGGGGAACACCCGCTGCTCTGGCCAAATTCGAGTCCCAATCTCCAGTCA 180
DB 277 TTCTTAGGGGAACACCCGCTGCTCTGGCCAAATTCGAGTCCCAATCTCCAGTCA 336
QY 181 TCACCAACCTGTTGCTCTCAATTTGCTGTTATCGCTGATGTTCTGGCGGTTTT 240
DB 337 TCACCAACCTGTTGCTCTCAATTTGCTGTTATCGCTGATGTTCTGGCGGTTTT 396
QY 241 ATCATCTCTCTGATCTCTGCTGCTATGCTCATCTCTGTTGTTCTTCTGACTAT 300
DB 397 ATCATCTCTCTGATCTCTGCTGCTATGCTCATCTCTGTTGTTCTTCTGACTAT 456
QY 301 CAAGGTATGTTGCGGTTGCTCTCAATTTGCTGATCAACACAGCAGCGGACCA 360
DB 457 CAAGGTATGTTGCGGTTGCTCTCAATTTGCTGATCAACACAGCAGCGGACCA 516
QY 361 TGCACCAACCTGCAACCTGCTGCTCAAGGAACCTCATGTTTCCCTCATGTTGCTG 420
DB 517 TGCACCAACCTGCAACCTGCTGCTCAAGGAACCTCATGTTTCCCTCATGTTGCTG 576
QY 421 AAACCTACGACGAGAAATCGACCTGATTTCCCATCCCATCATCTTGGGCTTTCG 480
DB 577 AAACCTACGACGAGAAATCGACCTGATTTCCCATCCCATCATCTTGGGCTTTCG 636

QY 481 TACCTATGGGAGTGGGCTCAGTCCGTTTCTTTGGCTCAGTTTACTAGTGCATTTGTT 540
DB 637 TACCTATGGGAGTGGGCTCAGTCCGTTTCTTTGGCTCAGTTTACTAGTGCATTTGTT 696
QY 541 CAGTGGTTCGTAGGCTTCCGCCACCTGCTGGGCTTTCAGTTATATGATGATGTTGTT 600
DB 697 CAGTGGTTCGTAGGCTTCCGCCACCTGCTGGGCTTTCAGTTATATGATGATGTTGTT 756
QY 601 TGGGGGCCAAGTCTGTACACATCTTGGTCCCTTTATGCCGCTGTTACCAATTTCTTT 660
DB 757 TGGGGGCCAAGTCTGTACACATCTTGGTCCCTTTATGCCGCTGTTACCAATTTCTTT 816
QY 661 TGTCTTTGGGTATACATTTAA 681
DB 817 TGTCTTTGGGTATACATTTAA 837

RESULT 5
US-10-453-792-283
; Sequence 283, Application US/10453792
; Publication No. US20040029110A1
; GENERAL INFORMATION:
; APPLICANT: STUYVER, LIEVEN
; ROSSAU, RUDI
; MAERTENS, GEERT
; TITLE OF INVENTION: METHOD FOR TYPING AND DETECTING HBV
; NUMBER OF SEQUENCES: 313
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHUYE P.C.
; STREET: 1100 NORTH GLEBE ROAD
; CITY: ARLINGTON
; STATE: VIRGINIA
; COUNTRY: U.S.A.
; ZIP: 22201-4714
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/453,792
; FILING DATE: 04-Jun-2003
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/155,885A
; FILING DATE: 08-Oct-1998
; APPLICATION NUMBER: PCT/EP97/02002
; FILING DATE: 21-Apr-1997
; APPLICATION NUMBER: EP 96870053.4
; FILING DATE: 19-Apr-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: SADOFF, B.J.
; REGISTRATION NUMBER: 36,663
; REFERENCE/DOCKET NUMBER: 2551-5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 816-4000
; TELEFAX: (703) 816-4100
; INFORMATION FOR SEQ ID NO: 283:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3221 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; SEQUENCE DESCRIPTION: SEQ ID NO: 283:
US-10-453-792-283

Query Match 93.9%; Score 639.4; DB 13; Length 3221;
Best Local Similarity 96.2%; Pred. No. 2.8e-198;
Matches 655; Conservative 0; Mismatches 26; Indels 0; Gaps 0;


```

RESULT 6
US-10-365-620-33
; Sequence 33, Application US/10365620
; Publication NO. US20040001853A1
; GENERAL INFORMATION:
; APPLICANT: George, Rajan
; APPLICANT: Tyrtell, Lorne
; APPLICANT: No US20040001853A1aim, Antoine
; TITLE OF INVENTION: Chimeric Antigens for Eliciting An Immune Response
; FILE REFERENCE: 656..0016
; CURRENT APPLICATION NUMBER: US/10/365.620
; CURRENT FILING DATE: 2003-02-13
; PRIOR APPLICATION NUMBER: US60/423.578
; PRIOR FILING DATE: 2003-11-05
; PRIOR APPLICATION NUMBER: 60/390,564
; PRIOR FILING DATE: 2002-06-20
; NUMBER OF SEQ ID NOS: 76
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 33
; LENGTH: 1365
; TYPE: DNA
; ORGANISM: Hepatitis B virus
US-10-365-620-33

```

```

RESULT 7
US-10-365-620-28
; Sequence 28, Application US/10365620
; Publication No. US20040001853A1
; GENERAL INFORMATION:
; APPLICANT: George, Rajan
; APPLICANT: Tyrrall, Lorne
; APPLICANT: No. US20040001853Aljaim, Antoine
; TITLE OF INVENTION: Chimeric Antigens for Eliciting An Immune Response
; FILE REFERENCES: 656.0016
; CURRENT APPLICATION NUMBER: US/10/365,620
; CURRENT FILING DATE: 2003-02-13
; PRIOR APPLICATION NUMBER: US60/423,578
; PRIOR FILING DATE: 2003-11-05
; PRIOR APPLICATION NUMBER: 60/390,564
; PRIOR FILING DATE: 2002-06-20
; NUMBER OF SEQ ID NOS: 76
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 28

```

; LENGTH: 2037
; TYPE: DNA
; ORGANISM: Hepatitis B virus
US-10-365-620-28

Query Match 92.9%; Score 632.6; DB 16; Length 2037;
Best Local Similarity 95.7%; Pred. No. 3.8e-196;
Matches 650; Conservative 0; Mismatches 29; Indels 0; Gaps 0;
QY 1 ATGAGAACATCGCATCAGGACTCCTAGGACCCCTGCTCGTGTATACAGGCGGGTTTTTC 60
DB 607 ATGAGAACATCATCAGGATTCCTAGGACCCCTGCTCGTGTATACAGGCGGGTTTTTC 666
QY 61 TTGTTGACAAATTCCTCAATACCGCAGAGTCTAGACTCGTGGTGGACTTCTCTCAAT 120
DB 667 TTGTTGACAAATTCCTCAATACCGCAGAGTCTAGACTCGTGGTGGACTTCTCTCAAT 726
QY 121 TTCTAGGGGGAACACCCGCTGTCTTGGCAAAATTCGAGTCCCAAAATTCAGTCCAC 180
DB 727 TTCTAGGGGGAACACCCGCTGTCTTGGCAAAATTCGAGTCCCAAAATTCAGTCCAC 786
QY 181 TCACCAACCTCTGCTCCTCAATTTGCTGGTATCGCTGGATGTCTGCGCGTTTTT 240
DB 787 TCACCAACCTCTGCTCCTCAATTTGCTGGTATCGCTGGATGTCTGCGCGTTTTT 846
QY 241 ATCATCTTCTCTGCTCCTCAATTTGCTGGTATCGCTGGATGTCTGCGCGTTTTT 300
DB 847 ATCATCTTCTCTGCTCCTCAATTTGCTGGTATCGCTGGATGTCTGCGCGTTTTT 906
QY 301 CAAGGTATGTTGCCCGTTTGTCTCAATTTGCTGGTATCGCTGGATGTCTGCGCGTTTTT 360
DB 907 CAAGGTATGTTGCCCGTTTGTCTCAATTTGCTGGTATCGCTGGATGTCTGCGCGTTTTT 966
QY 361 TGCARAACTGACAACTCTGCTCAAGGAACTCTATGTTCCCTCAATTTGCTGGTAT 420
DB 967 TGCARAACTGACAACTCTGCTCAAGGAACTCTATGTTCCCTCAATTTGCTGGTAT 1026
QY 421 AAACCTACGAGACAACTCTGCTCAAGGAACTCTATGTTCCCTCAATTTGCTGGTAT 480
DB 1027 AAACCTACGAGACAACTCTGCTCAAGGAACTCTATGTTCCCTCAATTTGCTGGTAT 1086
QY 481 TACCTATGGAGTGGGCTCAGTCCGTTTCTCTTGGCTCAGTTCATGATGATGTTT 540
DB 1087 TACCTATGGAGTGGGCTCAGTCCGTTTCTCTTGGCTCAGTTCATGATGATGTTT 1146
QY 541 CAGTGGTTCGTAGGGCTTTCCCGCTCAGTTCATGATGATGATGATGATGATGAT 600
DB 1147 CAGTGGTTCGTAGGGCTTTCCCGCTCAGTTCATGATGATGATGATGATGATGAT 1206
QY 601 TGGGGCCCAAGTCTGTACAACTCTGAGTCCCTTTATGCGCTGTATACCAATTTCTTT 660
DB 1207 TGGGGCCCAAGTCTGTACAACTCTGAGTCCCTTTATGCGCTGTATACCAATTTCTTT 1266
QY 661 TGTCTTTGGGTATACATTT 679
DB 1267 TGTCTTTGGGTATACATTT 1285

RESULT 8
US-10-365-620-31

; Sequence 31, Application US/10365620
; Publication No. US20040001853A1
; GENERAL INFORMATION:
; APPLICANT: George, Rajan
; APPLICANT: Tyrrell, Lorne
; APPLICANT: No. US20040001853A1, Antoine
; TITLE OF INVENTION: Chimeric Antigens for Eliciting An Immune Response
; FILE REFERENCE: 656.0016
; CURRENT APPLICATION NUMBER: US/10/365,620
; CURRENT FILING DATE: 2003-02-13
; PRIOR APPLICATION NUMBER: US60/423,578
; PRIOR FILING DATE: 2003-11-05
; PRIOR APPLICATION NUMBER: 60/390,564

; PRIOR FILING DATE: 2002-06-20
; NUMBER OF SEQ ID NOS: 76
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 31
; LENGTH: 2037
; TYPE: DNA
; ORGANISM: Hepatitis B virus
US-10-365-620-31

Query Match 92.9%; Score 632.6; DB 16; Length 2037;
Best Local Similarity 95.7%; Pred. No. 3.8e-196;
Matches 650; Conservative 0; Mismatches 29; Indels 0; Gaps 0;
QY 1 ATGAGAACATCGCATCAGGACTCCTAGGACCCCTGCTCGTGTATACAGGCGGGTTTTTC 60
DB 607 ATGAGAACATCATCAGGATTCCTAGGACCCCTGCTCGTGTATACAGGCGGGTTTTTC 666
QY 61 TTGTTGACAAATTCCTCAATACCGCAGAGTCTAGACTCGTGGTGGACTTCTCTCAAT 120
DB 667 TTGTTGACAAATTCCTCAATACCGCAGAGTCTAGACTCGTGGTGGACTTCTCTCAAT 726
QY 121 TTCTAGGGGGAACACCCGCTGTCTTGGCAAAATTCGAGTCCCAAAATTCAGTCCAC 180
DB 727 TTCTAGGGGGAACACCCGCTGTCTTGGCAAAATTCGAGTCCCAAAATTCAGTCCAC 786
QY 181 TCACCAACCTCTGCTCCTCAATTTGCTGGTATCGCTGGATGTCTGCGCGTTTTT 240
DB 787 TCACCAACCTCTGCTCCTCAATTTGCTGGTATCGCTGGATGTCTGCGCGTTTTT 846
QY 241 ATCATCTTCTCTGCTCCTCAATTTGCTGGTATCGCTGGATGTCTGCGCGTTTTT 300
DB 847 ATCATCTTCTCTGCTCCTCAATTTGCTGGTATCGCTGGATGTCTGCGCGTTTTT 906
QY 301 CAAGGTATGTTGCCCGTTTGTCTCAATTTGCTGGTATCGCTGGATGTCTGCGCGTTTTT 360
DB 907 CAAGGTATGTTGCCCGTTTGTCTCAATTTGCTGGTATCGCTGGATGTCTGCGCGTTTTT 966
QY 361 TGCARAACTGACAACTCTGCTCAAGGAACTCTATGTTCCCTCAATTTGCTGGTAT 420
DB 967 TGCARAACTGACAACTCTGCTCAAGGAACTCTATGTTCCCTCAATTTGCTGGTAT 1026
QY 421 AAACCTACGAGACAACTCTGCTCAAGGAACTCTATGTTCCCTCAATTTGCTGGTAT 480
DB 1027 AAACCTACGAGACAACTCTGCTCAAGGAACTCTATGTTCCCTCAATTTGCTGGTAT 1086
QY 481 TACCTATGGAGTGGGCTCAGTCCGTTTCTCTTGGCTCAGTTCATGATGATGATGAT 540
DB 1087 TACCTATGGAGTGGGCTCAGTCCGTTTCTCTTGGCTCAGTTCATGATGATGATGAT 1146
QY 541 CAGTGGTTCGTAGGGCTTTCCCGCTCAGTTCATGATGATGATGATGATGATGAT 600
DB 1147 CAGTGGTTCGTAGGGCTTTCCCGCTCAGTTCATGATGATGATGATGATGATGAT 1206
QY 601 TGGGGCCCAAGTCTGTACAACTCTGAGTCCCTTTATGCGCTGTATACCAATTTCTTT 660
DB 1207 TGGGGCCCAAGTCTGTACAACTCTGAGTCCCTTTATGCGCTGTATACCAATTTCTTT 1266
QY 661 TGTCTTTGGGTATACATTT 679
DB 1267 TGTCTTTGGGTATACATTT 1285

RESULT 9

US-10-267-922-15
; Sequence 15, Application US/10267922
; Publication No. US20030143527A1
; GENERAL INFORMATION:
; APPLICANT: SHYAMALA, Venkatakrishna
; TITLE OF INVENTION: IDENTIFICATION OF OLIGONUCLEOTIDES FOR THE CAPTURE,
; TITLE OF INVENTION: DETECTION AND QUANTIFICATION OF HEPATITIS B VIRAL DNA
; FILE REFERENCE: 2301-18346 / PPI8346.004
; CURRENT APPLICATION NUMBER: US/10/267,922
; CURRENT FILING DATE: 2002-10-09

NUMBER OF SEQUENCES: 313
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERHUYE P.C.
STREET: 1100 NORTH GLEBE ROAD
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: U.S.A.
ZIP: 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/453,792
FILING DATE: 04-Jun-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/155,885A
FILING DATE: 08-Oct-1998
APPLICATION NUMBER: PCT/EP97/02002
FILING DATE: 21-APR-1997
APPLICATION NUMBER: EP 96870053.4
FILING DATE: 19-APR-1996
ATTORNEY/AGENT INFORMATION:
NAME: SADOFF, B.J.
REGISTRATION NUMBER: 36,663
REFERENCE/DOCKET NUMBER: 2551-5
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 816-4000
TELEFAX: (703) 816-4100
INFORMATION FOR SEQ ID NO: 280:
SEQUENCE CHARACTERISTICS:
LENGTH: 3200 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
SEQUENCE DESCRIPTION: SEQ ID NO: 280:

397	ATCATATTCTCTTCATCTCGTCTGCTATGCTCATCTTCTATTGGTTCTCTGGATTAT	456
Db		
301	CAAGGTATGTGCGCGTTTGTCTCTAAATTCAGGATCAACAACACGACCGGACCA	360
Qy		
457	CAAGGTATGTGCGCGTTTGTCTCTAAATTCAGGATCAACAACACGATCGGGACCA	516
Db		
361	TGCAAAACCTGGACAATCTCTGCTCAAGGAACCTCTATGTTTCCTCATGTTCTGTACA	420
Qy		

Db 517 TGAACAACTGCACGACTCCTGCTCAAGGCAACTCTAAGTTTCCTCATGTTGCTGTACA 576
Qy 421 AAACCTACGGACAGAACTGCACCTGTATTCCTCAATCCATCATCTTGGGCTTTTCGAAAA 480
Db 577 AAACCTACGGATGAAATTCACCTGTATTCCTCAATCCATCATCTTGGGCTTTTCGAAAA 636
Qy 481 TACCTATGGAGTGGGCTCAGTCCGTTCTCTTGGCTCAGTTTACTAGTGCCATTGTT 540
Db 637 TACCTATGGAGTGGGCTCAGTCCGTTCTCTTGGCTCAGTTTACTAGTGCCATTGTT 696
Qy 541 CAGTGGTTCGTAGGGCTTTCCCCCACTGTCTGGCTTTTCACTATATGGATGATGTGTT 600
Db 697 CAGTGGTTCGTAGGGCTTTCCCCCACTGTCTGGCTTTTCACTATATGGATGATGTGTT 756
Qy 601 TGGGGGCAAGTCTGTACAACTCTGAGTCCCTTTATGCGCTGTATCCAAATTTCTTT 660
Db 757 TGGGGGCAAGTCTGTACAACTCTGAGTCCCTTTATGCGCTGTATCCAAATTTCTTT 816
Qy 661 TGTCTTTGGGTATACATTTAA 681
Db 817 TGTCTCTGGGTATACATTTAA 837

RESULT 11

US-10-453-792-279
; Sequence 279, Application US/10453792
; Publication No. US20040029110A1
; GENERAL INFORMATION:
; APPLICANT: STUYVER, LIEVEN
; ROSSAU, RUDI
; MAERTENS, GEERT
; TITLE OF INVENTION: METHOD FOR TYPING AND DETECTING HBV
; NUMBER OF SEQUENCES: 313
; CORRESPONDENCE ADDRESS:
; ADDRESS: NIXON & VANDERVE P.C.
; STREET: 1100 NORTH GLEBE ROAD
; CITY: ARLINGTON
; STATE: VIRGINIA
; COUNTRY: U.S.A.
; ZIP: 22201-4714
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30 (BPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/453,792
; FILING DATE: 04-Jun-2003
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/155,885A
; FILING DATE: 08-Oct-1998
; APPLICATION NUMBER: PCT/EP97/02002
; FILING DATE: 21-APR-1997
; APPLICATION NUMBER: EP 96870053.4
; FILING DATE: 19-APR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: SADOFF, B.J.
; REGISTRATION NUMBER: 36,663
; REFERENCE/DOCKET NUMBER: 2551-5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 816-4000
; TELEFAX: (703) 816-4100
; INFORMATION FOR SEQ ID NO: 279:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3221 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO

US-10-453-792-279

Query Match 92.7%; Score 631.4; DB 13; Length 3221;
Best Local Similarity 95.4%; Pred. No. 1.2e-195;
Matches 650; Conservative 0; Mismatches 31; Indels 0; Gaps 0;
Qy 1 ATGGAGACATCGCATCAGGACTCTAGGACCCCTGCTCGTTTACAGGCGGGGTTTTTC 60
Db 157 ATGGAGACATCACAATCAGGATTCCTAGGACCCCTGCTCGTTTACAGGCGGGGTTTTTC 216
Qy 61 TTGTTGACAAAAATCCTCACAATACCGCAGAGTCTAGACTCGTGGTGGACTTCTCTCAAT 120
Db 217 TTGTTGACAGAATCCTCACAATACCGCAGAGTCTAGACTCGTGGTGGACTTCTCTCAAT 276
Qy 121 TTTCTAGGGGGAACACCCGCTGTCTTGGCCAAAATTCGAGTCCGAAATCTCCAGTCAC 180
Db 277 TTTCTAGGGGGAACACCCGCTGTCTTGGCCAAAATTCGAGTCCGAAATCTCCAGTCAC 336
Qy 181 TCACCAACTCTGTGTCCTCCAAATTTGCTGCTTATCGCTGGATGTGTCTGCGCGCTTTT 240
Db 337 TCACCAACTCTGTGCTCCAAATTTGCTGCTTATCGCTGGATGTGTCTGCGCGCTTTT 396
Qy 241 ATCAFTTCTCTGCTGCTGCTGCTATGCTGCTATGCTGCTATGCTTCTTCTTGGACTAT 300
Db 397 ATCATATTTCTCTTCACTGCTGCTATGCTGCTATGCTTCTTCTTCTTGGACTAT 456
Qy 301 CAAGGTATGTTGCCCGTTTGTCTCTAATTCAGAGTCAACAACACAGCAGCAGGACCA 360
Db 457 CAAGGTATGTTGCCCGTTTGTCTCTAATTCAGAGTCAACAACACAGCAGCAGGACCA 516
Qy 361 TCGAAAACTGCACAACTCTGCTCAAGGAACTCTATGTTTCCCTCATGTTGCTGTACA 420
Db 517 TCGAAAACTGCACAACTCTGCTCAAGGCAACTCTATGTTTCCCTCATGTTGCTGTACA 576
Qy 421 AAACCTACGGACAGAACTGCACCTGTATTCCTCAATCCATCCATCTTGGGCTTTTCGAAAA 480
Db 577 AAACCTACGGATGAAATTCGACCTGTATTCCTCAATCCATCCATCTTGGGCTTTTCGAAAA 636
Qy 481 TACCTATGGAGTGGGCTCAGTCCGTTTCTCTTGGCTCAGTTTACTAGTGCCATTGTT 540
Db 637 TACCTATGGAGTGGGCTCAGTCCGTTTCTCTTGGCTCAGTTTACTAGTGCCATTGTT 696
Qy 541 CAGTGGTTCGTAGGGCTTTCCCCCACTGTCTGGCTTTTCACTATATGGATGATGTGTT 600
Db 697 CAGTGGTTCGTAGGGCTTTCCCCCACTGTCTGGCTTTTCACTATATGGATGATGTGTT 756
Qy 601 TGGGGGCAAGTCTGTACAACTCTTCACTGCTCCCTTTATGCGCTGTATCCAAATTTCTTT 660
Db 757 TGGGGGCAAGTCTGTACAACTCTTCACTGCTCCCTTTATGCGCTGTATCCAAATTTCTTT 816
Qy 661 TGTCTTTGGGTATACATTTAA 681
Db 817 TGTCTCTGGGTATACATTTAA 837

RESULT 12

US-09-781-891D-21
; Sequence 21, Application US/09781891D
; Publication No. US2003009622A1
; GENERAL INFORMATION:
; APPLICANT: Delaney, William IV
; APPLICANT: Locarnini, Stephen Alister
; APPLICANT: Chen, Robert Yung Ming
; APPLICANT: Bartholomeusz, Angelina
; APPLICANT: Isom, Harriet
; TITLE OF INVENTION: An assay
; FILE REFERENCE: 2378750/EJH
; CURRENT APPLICATION NUMBER: US/09/781,891D
; CURRENT FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 60/179,948
; PRIOR FILING DATE: 2000-02-03
; NUMBER OF SEQ ID NOS: 22

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; SEQ ID NO 21
; LENGTH: 4084
; TYPE: DNA
; ORGANISM: HBV 1.28 genome
US-09-781-891D-21

Query Match      92.7%; Score 631.4; DB 10; Length 4084;
Best Local Similarity 95.4%; Pred. No. 1.3e-195;
Matches 650; Conservative 0; Mismatches 31; Indels 0; Gaps 0;

QY 1 ATGAGAACATCGCATCAGACATCCCTAGGACCCCTGCTGTTACAGCGGGGTTTTC 60
Db 1925 ATGAGAACATCACATCAGGATTCCTAGGACCCCTGCTGTTACAGCGGGGTTTTC 1984

QY 61 TTGTTGACAAAATCTCTCAATACCGAGAGTCTAGACTCGTGGTGGACTTCTCTCAAT 120
Db 1985 TTGTTGACAAAATCTCTCAATACCGAGAGTCTAGACTCGTGGTGGACTTCTCTCAAT 2044

QY 121 TTTCTAGGGGAAACACCGGTGTCTTGGCCAAAATTCGCAGTCCCAATCTCCAGTCA 180
Db 2045 TTTCTAGGGGAAATCTCCGGTGTCTTGGCCAAAATTCGCAGTCCCAATCTCCAGTCA 2104

QY 181 TCACCAACCTGTTGCTCTCCAAATTTGCTGTTATCGCTGGATGTTTGGGGGTTT 240
Db 2105 TCACCAACCTGTTGCTCTCCAAATTTGCTGTTATCGCTGGATGTTTGGGGGTTT 2164

QY 241 ATCATCTTCTGCTGATCTGCTGCTATGCTCATCTTCTGTTCTTCTGGACTAT 300
Db 2165 ATCATATTCCTGCTGATCTGCTGCTATGCTCATCTTCTGTTCTTCTGGACTAT 2224

QY 301 CAAAGTATGTTGGCCGTTTGTCTCTAAATTCAGGATCAACAAACACCGAGACCA 360
Db 2225 CAAAGTATGTTGGCCGTTTGTCTCTAAATTCAGGATCAACAAACACCGAGACCA 2284

QY 361 TGCAAAACCTGCAACATCTGCTCAAGGAACCTCTATGTTTCCCTCATGTTGCTGTACA 420
Db 2285 TGCAAAACCTGCAACATCTGCTCAAGGAACCTCTATGTTTCCCTCATGTTGCTGTACA 2344

QY 421 ABACTTACGACAGAAATGCACTGATTTCCATCCCATCATCTTGGCTTTCGCAAAA 480
Db 2345 ABACTTACGACAGAAATGCACTGATTTCCATCCCATCATCTTGGCTTTCGCAAAA 2404

QY 481 TACCTATGGAGTGGGCTCAGTCCGTTTCTTGTGCTCAGTTTACTAGTGCATTTGTT 540
Db 2405 TACCTATGGAGTGGGCTCAGTCCGTTTCTTGTGCTCAGTTTACTAGTGCATTTGTT 2464

QY 541 CAGTGGTTCGTAGGGCTTTCCCGACTGTTCCAGTCTGCTGATATGATGTTGTTT 600
Db 2465 CAGTGGTTCGTAGGGCTTTCCCGACTGTTCCAGTCTGCTGATATGATGTTGTTT 2524

QY 601 TGGGGGCCAAGTCTGTACACATCTTTCAGTCCCTTTATGCGGCTGTTACCAATTTTCTTT 660
Db 2525 TGGGGGCCAAGTCTGTACACATCTTTCAGTCCCTTTATGCGGCTGTTACCAATTTTCTTT 2584

QY 661 TGCTCTGGGTATACATTTAA 681
Db 2585 TGCTCTGGGTATACATTTAA 2605

RESULT 13
US-09-781-891D-22
; Sequence 22, Application US/09781891D
; Publication No. US2003009622A1
; GENERAL INFORMATION:
; APPLICANT: Delaney, William IV
; APPLICANT: Locarnini, Stephen Alister
; APPLICANT: Chen, Robert Yung Ming
; APPLICANT: Bartholomeusz, Angeline
; APPLICANT: Isom, Harriet
; TITLE OF INVENTION: An assay
; FILE REFERENCE: 2378750/EJH
; CURRENT APPLICATION NUMBER: US/09/781.891D
; CURRENT FILING DATE: 2001-02-02
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; PRIOR APPLICATION NUMBER: 60/179,948
; PRIOR FILING DATE: 2000-02-03
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 22
; LENGTH: 4496
; TYPE: DNA
; ORGANISM: HBV 1.5 genome
US-09-781-891D-22

Query Match      92.7%; Score 631.4; DB 10; Length 4496;
Best Local Similarity 95.4%; Pred. No. 1.4e-195;
Matches 650; Conservative 0; Mismatches 31; Indels 0; Gaps 0;

QY 1 ATGAGAACATCGCATCAGACATCCCTAGGACCCCTGCTGTTACAGCGGGGTTTTC 60
Db 2337 ATGAGAACATCACATCAGGATTCCTAGGACCCCTGCTGTTACAGCGGGGTTTTC 2396

QY 61 TTGTTGACAAAATCTCTCAATACCGAGAGTCTAGACTCGTGGTGGACTTCTCTCAAT 120
Db 2397 TTGTTGACAAAATCTCTCAATACCGAGAGTCTAGACTCGTGGTGGACTTCTCTCAAT 2456

QY 121 TTTCTAGGGGAAACACCGGTGTCTTGGCCAAAATTCGCAGTCCCAATCTCCAGTCA 180
Db 2457 TTTCTAGGGGAAATCTCCGGTGTCTTGGCCAAAATTCGCAGTCCCAATCTCCAGTCA 2516

QY 181 TCACCAACCTGTTGCTCTCCAAATTTGCTGTTATCGCTGGATGTTTGGGGGTTT 240
Db 2517 TCACCAACCTGTTGCTCTCCAAATTTGCTGTTATCGCTGGATGTTTGGGGGTTT 2576

QY 241 ATCATCTTCTGCTGATCTGCTGCTATGCTCATCTTCTTATTTGGTTCTTCTGGACTAT 300
Db 2577 ATCATATTCCTGCTGATCTGCTGCTATGCTCATCTTCTTATTTGGTTCTTCTGGACTAT 2636

QY 301 CAAAGTATGTTGGCCGTTTGTCTCTAAATTCAGGATCAACAAACACCGAGACCA 360
Db 2637 CAAAGTATGTTGGCCGTTTGTCTCTAAATTCAGGATCAACAAACACCGAGACCA 2696

QY 361 TGCAAAACCTGCAACATCTGCTCAAGGAACCTCTATGTTTCCCTCATGTTGCTGTACA 420
Db 2697 TGCAAAACCTGCAACATCTGCTCAAGGAACCTCTATGTTTCCCTCATGTTGCTGTACA 2756

QY 421 AAACCTACGACAGAAATGCACTGATTTCCATCCCATCATCTTGGCTTTCGCAAAA 480
Db 2757 AAACCTACGACAGAAATGCACTGATTTCCATCCCATCATCTTGGCTTTCGCAAAA 2816

QY 481 TACCTATGGAGTGGGCTCAGTCCGTTTCTTGTGCTCAGTTTACTAGTGCATTTGTT 540
Db 2817 TACCTATGGAGTGGGCTCAGTCCGTTTCTTGTGCTCAGTTTACTAGTGCATTTGTT 2876

QY 541 CAGTGGTTCGTAGGGCTTTCCCGACTGTTCCAGTCTGCTGATATGATGTTGTTT 600
Db 2877 CAGTGGTTCGTAGGGCTTTCCCGACTGTTCCAGTCTGCTGATATGATGTTGTTT 2936

QY 601 TGGGGGCCAAGTCTGTACACATCTTTCAGTCCCTTTATGCGGCTGTTACCAATTTTCTTT 660
Db 2937 TGGGGGCCAAGTCTGTACACATCTTTCAGTCCCTTTATGCGGCTGTTACCAATTTTCTTT 2996

QY 661 TGCTCTGGGTATACATTTAA 681
Db 2997 TGCTCTGGGTATACATTTAA 3017

RESULT 14
US-10-453-792-304
; Sequence 304, Application US/10453792
; Publication No. US20040029110A1
; GENERAL INFORMATION:
; APPLICANT: STUYVER, LIEVEN
; APPLICANT: ROSSAU, RUDI
; APPLICANT: MAERTENS, GEERT
; TITLE OF INVENTION: METHOD FOR TYPING AND DETECTING HBV
; NUMBER OF SEQUENCES: 313
```

CORRESPONDENCE ADDRESS:
 ADDRESSEE: NIXON & VANDERHYE P.C.
 STREET: 1100 NORTH GLEBE ROAD
 CITY: ARLINGTON
 STATE: VIRGINIA
 COUNTRY: U.S.A.
 ZIP: 22201-4714
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/10/453,792
 FILING DATE: 04-Jun-2003
 CLASSIFICATION: <Unknown>
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US/09/155,885A
 FILING DATE: 08-Oct-1998
 APPLICATION NUMBER: PCT/EP97/02002
 FILING DATE: 21-APR-1997
 APPLICATION NUMBER: EP 96870053.4
 FILING DATE: 19-APR-1996
 ATTORNEY/AGENT INFORMATION:
 NAME: SADOFF, B. J.
 REGISTRATION NUMBER: 36,663
 REFERENCE/DOCKET NUMBER: 2551-5
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (703) 816-4000
 TELEFAX: (703) 816-4100
 INFORMATION FOR SEQ ID NO: 304:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 3182 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)
 HYPOTHETICAL: NO
 ANTI-SENSE: NO
 SEQUENCE DESCRIPTION: SEQ ID NO: 304:
 US-10-453-792-304

Query Match 92.5%; Score 629.8; DB 13; Length 3182;
 Best Local Similarity 95.3%; Pred. No. 3.9e-195;
 Matches 649; Conservative 0; Mismatches 32; Indels 0; Gaps 0;
 QY 1 ATGAGAACATCCGATCAGGACTCCCTAGGACCCCTGCTGTTACAGCGGGGTTTTTC 60
 DB 157 ATGAGAACATCAGATCAGGATTCCTAGGACCCCTGCTGTTACAGCGGGGTTTTTC 216
 QY 61 TTGTTGACAAAATCCTCAATAACCGCAGAGTCTAGACTCGTGGTGGACTTCTCTCAAT 120
 DB 217 TTGTTGACAGAAATCCTCAATAACCGCAGAGTCTAGACTCGTGGTGGACTTCTCTCAAT 276
 QY 121 TTCTAGGGGGAACACCGGTGTCTTGGCCAAAATTCGACGTCCCAATCTCCAGTCAAC 180
 DB 277 TTCTAGGGGGAACACTACCGGTGTCTTGGCCAAAATTCGACGTCCCAATCTCCAGTCAAC 336
 QY 181 TCACCAACCTGTGTCCTCAATTCCTGTTATCGCTGGATGTCTGCGGGGTTTTT 240
 DB 337 TCACCAACCTGTGTCCTCAATTCCTGTTATCGCTGGATGTCTGCGGGGTTTTT 396
 QY 241 ATCATCTTCTCTGCAATCTGCTGATGCTCATCTTCTGTTGTTCTTCTGCACTAT 300
 DB 397 ATCATCTTCTCTGCAATCTGCTGATGCTCATCTTCTGTTGTTCTTCTGCACTAT 456
 QY 301 CAAGGTATGTGCGCGTTGTCCTCAATTCCTGTTATCGCTGGATGTCTGCGGGGTTTTT 360
 DB 457 CAAGGTATGTGCGCGTTGTCCTCAATTCCTGTTATCGCTGGATGTCTGCGGGGTTTTT 516
 QY 361 TGCAAAACCTGCAACACTGCTGCTCAAGGAACTCTATGTTTCCCTCATGTTGCTGTACA 420
 DB 517 TGCAGAACCTGCAACACTGCTGCTCAAGGAACTCTATGTTTCCCTCATGTTGCTGTACC 576

QY 421 AAACCTACGGACAGAAACTGCACCTGTATTCCCATCCCATCATCTTGGGCTTTCCGAAA 480
 DB 577 AAACCTTCGGACGGAAATTCACCTGTATTCCCATCCCATCATCTTGGGCTTTCCGAAA 636
 QY 481 TACCTATGGAGTGGGCTCAGTCCGTTTCTCTTGGCTCAGTTTACTAGTGCATTTGTT 540
 DB 637 TTCCTATGGAGTGGGCTCAGTCCGTTTCTCTTGGCTCAGTTTACTAGTGCATTTGTT 696
 QY 541 CAGTGGTTCTGATGGGCTTTTCCCCACACTGTCTGGCTTTTTCAGTTATATGATGATGTGTT 600
 DB 697 CAGTGGTTCTGATGGGCTTTTCCCCACACTGTCTGGCTTTTTCAGTTATATGATGATGTGTT 756
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 DB 757 TGGGGGCCAAGTCTGTACAAATCTTGGTCCCTTTTATGGCGCTGTACCAATTTCTTT 816
 QY 661 TGTCTTGGGTATACATTTAA 681
 DB 817 TGTCTTGGGTATACATTTAA 837
 RESULT 15
 US-09-821-877-3
 ; Sequence 3, Application US/09821877
 ; Patent No. US2002017124A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Abbott Laboratories
 ; APPLICANT: Coleman, Paul F.
 ; APPLICANT: Mushahwar, Isa K.
 ; TITLE OF INVENTION: Hepatitis B Virus Surface Antigen Mutant
 ; TITLE OF INVENTION: And Methods Of Detection Thereof
 ; FILE REFERENCE: 6794.US.01
 ; CURRENT APPLICATION NUMBER: US/09/821,877
 ; CURRENT FILING DATE: 2000-03-03
 ; NUMBER OF SEQ ID NOS: 8
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 3
 ; LENGTH: 681
 ; TYPE: DNA
 ; ORGANISM: Hepatitis B Virus
 US-09-821-877-3

Query Match 92.2%; Score 628.2; DB 9; Length 681;
 Best Local Similarity 95.2%; Pred. No. 5.9e-195;
 Matches 648; Conservative 0; Mismatches 33; Indels 0; Gaps 0;
 QY 1 ATGAGAACATCGGATCAGGACTCCCTAGGACCCCTGCTGTTACAGCGGGGTTTTTC 60
 DB 1 ATGAGAACATCATCAGGATTCCTAGGACCCCTGCTGTTACAGCGGGGTTTTTC 60
 QY 61 TTGTTGACAAAATCCTCAATAACCGCAGAGTCTAGACTCGTGGTGGACTTCTCTCAAT 120
 DB 61 TTGTTGACAGAAATCCTCAATAACCGCAGAGTCTAGACTCGTGGTGGACTTCTCTCAAT 120
 QY 121 TTCTAGGGGGAACACCGGTGTCTTGGCCAAAATTCGACGTCCCAATCTCCAGTCAAC 180
 DB 121 TTCTAGGGGGAACACTACCGGTGTCTTGGCCAAAATTCGACGTCCCAATCTCCAGTCAAC 180
 QY 181 TCACCAACCTGTGTCCTCAATTCCTGTTATCGCTGGATGTCTGCGGGGTTTTT 240
 DB 181 TCACCAACCTGTGTCCTCAATTCCTGTTATCGCTGGATGTCTGCGGGGTTTTT 240
 QY 241 ATCATCTTCTCTGCAATCTGCTGATGCTCATCTTCTGTTGTTCTTCTGCACTAT 300
 DB 241 ATCATCTTCTCTGCAATCTGCTGATGCTCATCTTCTGTTGTTCTTCTGCACTAT 300
 QY 301 CAAGGTATGTGCGCGTTGTCCTCAATTCCTGTTATCGCTGGATGTCTGCGGGGTTTTT 360
 DB 301 CAAGGTATGTGCGCGTTGTCCTCAATTCCTGTTATCGCTGGATGTCTGCGGGGTTTTT 360
 QY 361 TGCAAAACCTGCAACACTGCTGCTCAAGGAACTCTATGTTTCCCTCATGTTGCTGTACA 420

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Db 361 TGCAGAACCTGCACGACTCCTGCTCAAGGAACCTCTATGTATCCCTCCTGTTGCTGTACA 420
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Db 421 AAACCTTCGGATGGAAACTGCACCTGTATTCCTATCCCATCCCATCATCTTGGGCTTTCGCAAAA 480
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Db 481 TTCCATATGGAGTGGGCTCAGCCGCTTCTCTTGGCTCAGTTTACTAGTGCCATTGTT 540
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Db 541 CAGTGTTCGTAGGGCTTTCCTCCCACTGTCTGGCTTTCAGTTATATGGATGATGGTTT 600
QY 601 TGGGGGCCAAGTCTGTACAACTCTTGGTTCCTTTATGCCGTGTATACCAATTTTCCTT 660
Db 601 TGGGGGCCAAGTCTGTACAACTCTTGGTTCCTTTTACCGCTGTATACCAATTTTCCTT 660
QY 661 TGTCTTTGGGTATACATTTAA 681
Db 661 TGTCTTTGGGTATACATTTAA 681
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Search completed: July 26, 2004, 16:40:02
Job time : 412 secs

OM nucleic - nucleic search, using sw model

Run on: July 26, 2004, 13:24:04 ; Search time 2410 Seconds
(without alignments)
8438.234 Million cell updates/sec

Title: US-09-719-533A-1_COPY_155_835

Perfect score: 681
Sequence: 1 ATGGAGACATCGCATCAGG.....GTCCTTGGGTATACATTAA 681

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:*
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2: em_estbua:*
3: em_estcin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_hic:*
9: gb_est1:*
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12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfum:*
16: em_estom:*
17: em_ges_hum:*
18: em_ges_inv:*
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20: em_ges_vrt:*
21: em_ges_fun:*
22: em_ges_mam:*
23: em_ges_mus:*
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25: em_ges_rod:*
26: em_ges_phg:*
27: em_ges_vrl:*
28: gb_ges1:*
29: gb_ges2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	41.2	6.0	997	29	CNS005TE
2	40.6	6.0	1201	13	BX376097
3	40.4	5.9	1201	13	BX460099
4	40	5.9	258	9	AV717959

C 5	40	5.9	258	9	AV717967
C 6	40	5.9	262	9	AV717947
C 7	40	5.9	264	9	AV717948
C 8	40	5.9	268	9	AV717975
C 9	40	5.9	269	9	AV717986
C 10	40	5.9	270	9	AV717995
C 11	40	5.9	270	9	AV718017
C 12	40	5.9	271	9	AV717964
C 13	40	5.9	300	9	AV717969
C 14	40	5.9	301	9	AV718014
C 15	40	5.9	301	9	AV718019
C 16	40	5.9	310	9	AV717951
C 17	40	5.9	314	9	AV718022
C 18	40	5.9	315	9	AV717996
C 19	40	5.9	334	9	AV718004
C 20	39.8	5.8	520	28	BZ128636
C 21	39.8	5.8	636	28	AZ038456
C 22	39.6	5.8	1200	9	AL576292
C 23	39.6	5.8	1201	9	AL563860
C 24	38.2	5.8	802	12	EG921060
C 25	38.2	5.8	922	13	BX332924
C 26	39	5.7	382	10	BE003197
C 27	38.8	5.7	1167	29	CNS04X6K
C 28	38.6	5.7	611	14	CB580512
C 29	38.6	5.7	628	13	BX482821
C 30	38.6	5.7	1155	10	BF570907
C 31	38.4	5.6	239	10	BF778098
C 32	38.4	5.6	264	9	AV717955
C 33	38.4	5.6	409	9	AI113181
C 34	38.4	5.6	621	12	BM492837
C 35	38.4	5.6	705	12	BM902701
C 36	38.2	5.6	214	9	AI053945
C 37	38.2	5.6	528	10	BE978648
C 38	38.2	5.6	598	29	CE376635
C 39	38	5.6	312	9	AV718005
C 40	38	5.6	1159	13	BX394939
C 41	37.8	5.6	887	13	BU217345
C 42	37.6	5.5	397	14	T89211
C 43	37.6	5.5	918	13	BQ710077
C 44	37.6	5.5	1085	12	EG293693
C 45	37.6	5.5	1101	29	CNS01844

ALIGNMENTS

RESULT 1
CNS005TE
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL

CNS005TE 997 bp DNA linear GSS 03-JUN-1999
Drosophila melanogaster genome survey sequence TET3 end of BAC #
BACR12K22 of RPCI-98 library from Drosophila melanogaster (fruit fly), genomic survey sequence.

AL060767
AL060767.1 GI:4943573
GSS.

Drosophila melanogaster (fruit fly)
Drosophila melanogaster

Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.

1 (bases 1 to 997)

Genoscope.

Direct Submission

Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :

BP 191 91006 EVRY cedex - FRANCE (E-mail : secref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)

Determination of this BAC-end sequence was carried out as part of a
collaboration with the Berkeley Drosophila Genome Project (BDGP).
The BDGP is constructing a physical map of the Drosophila
melanogaster genome using these BACs. For further information
please see <http://www.fruitfly.org> The BDGP Drosophila
melanogaster BAC library was prepared by Kazutoyo Osogawa and
Aaron Mammose in Pieter de Jong's laboratory in the Department of

Email: seqrefgenoscope.cns.fr, Web: www.genoscope.cns.fr
Library was constructed by Life technologies, a division of
Invitrogen. Contact: Feng Liang Email: fliang@lifetech.com URL:
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Paraday Avenue Genoscope sequence ID: CS0DF010DH06QPI.

FEATURES
Source
1. 1201
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DF010YPI2"
/tissue type="FETAL BRAIN"
/dev stage="fetal"
/clone lib="Homo sapiens FETAL BRAIN"
/note="Organ: brain; Vector: pCMVSPORT 6; 1st strand cDNA
was primed with a NotI-oligo(dT) primer. Five prime end
enriched, double-strand cDNA was digested with Not I and
cloned into the Not I and EcoRV sites of the pCMVSPORT 6
vector. Library was not normalized."

ORIGIN
Query Match 5.9%; Score 40.4; DB 13; Length 1201;
Best Local Similarity 8.4%; Pred. No. 6.5; Mismatches 111; Indels 0; Gaps 0;
Matches 23; Conservative 139;
QY 260 TGCTGCTATGCTTCATCTCTTCTTCTGCTTCTTCTGACTATCAAGTATGTTGCCCGTTT 319
Db 1128 KMMVMYKGGKK 1069
QY 320 GTCTCTTAATTCAGGATCAACACACGACGACGACGACGACGACGACGACGACGACGAC 379
Db 1068 DKNAKAKDKKK 1009
QY 380 CTGCTCAAGAACTCTATGTTTCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 439
Db 1008 BKGGCMKMKKRCBMMKK 949
QY 440 GCACCTGTATTCACATCCATCTTCTGCTTCTGCTTCTGCTTCTGCTTCTGCTTCTGCTT 499
Db 948 KKKMMAMCKMYBMMBMMBMMBMMBMMBMMBMMBMMBMMBMMBMMBMMBMMBMMBMMBMM 889
QY 500 CAGTCGCTTCTCTTGGCTCAGTTTACTAGTC 532
Db 888 GKXKMKKK 856

RESULT 4
AV717959/c
LOCUS AV717959 GK Homo sapiens cDNA clone FGKAB05.5, mRNA sequence.
DEFINITION AV717959
ACCESSION AV717959
VERSION AV717959.2 GI:37805005
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 258)
AUTHORS Wu,T., Qian,B., Huang,Q., Kang,B., Gao,X., Xu,Z.,
Xiao,H., Xu,X., Li,N., Peng,Y., Liu,F., Ou,J., Song,H., Cheng,Z.,
Zeng,L., Xu,S., Gu,W., Tu,Y., Jia,J., Fu,G., Ren,S., Zhong,M.,
Lu,G., Yang,Y., Gu,Y., Chen,Z. and Han,Z.
TITLE Homo sapiens cDNA GK clones
JOURNAL Unpublished (2000)
COMMENT On Oct 16, 2000 this sequence version replaced gi:10815111.
Contact: Zeguang Han
Chinese National Human Genome Center at Shanghai
351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
201203, P. R. China
Tel: 86-21-50801919(ex. 45)
Fax: 86-21-50801922
Email: hanzg@chgc.sh.cn
This clone is available at CHGC in Shanghai.

FEATURES
source
1. 258
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="FGKAB05"
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/note="Vector: pBluescript sk(-); Site_1: EcoRI; Site_2:
XhoI"

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Best Local Similarity 100.0%; Pred. No. 4.8;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 496 GCCTCAGTCGCTTCTTCTTGGCTCAGTTTACTAGTGCCAT 535
Db 258 GCCTCAGTCGCTTCTTCTTGGCTCAGTTTACTAGTGCCAT 219

RESULT 5
AV717967/c
LOCUS AV717967 GK Homo sapiens cDNA clone FGKAB02.5, mRNA sequence.
DEFINITION AV717967
ACCESSION AV717967
VERSION AV717967.2 GI:37805013
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 258)
AUTHORS Wu,T., Qian,B., Huang,Q., Kang,B., Gao,X., Xu,Z.,
Xiao,H., Xu,X., Li,N., Peng,Y., Liu,F., Ou,J., Song,H., Cheng,Z.,
Zeng,L., Xu,S., Gu,W., Tu,Y., Jia,J., Fu,G., Ren,S., Zhong,M.,
Lu,G., Yang,Y., Gu,Y., Chen,Z. and Han,Z.
TITLE Homo sapiens cDNA GK clones
JOURNAL Unpublished (2000)
COMMENT On Oct 16, 2000 this sequence version replaced gi:10815119.
Contact: Zeguang Han
Chinese National Human Genome Center at Shanghai
351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
201203, P. R. China
Tel: 86-21-50801919(ex. 45)
Fax: 86-21-50801922
Email: hanzg@chgc.sh.cn
This clone is available at CHGC in Shanghai.

FEATURES
source
1. 258
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/db_xref="taxon:9606"
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/lab_host="SOLR"
/clone lib="GK"
/note="Vector: pBluescript sk(-); Site_1: EcoRI; Site_2:
XhoI"

ORIGIN
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Best Local Similarity 100.0%; Pred. No. 4.8;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 496 GCCTCAGTCGCTTCTTCTTGGCTCAGTTTACTAGTGCCAT 535
Db 257 GCCTCAGTCGCTTCTTCTTGGCTCAGTTTACTAGTGCCAT 218

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RESULT 6
AV717947/c
LOCUS AV717947 GK Homo sapiens cDNA clone FGKABAH01 5', mRNA linear EST 21-OCT-2003
DEFINITION AV717947 GK Homo sapiens cDNA clone FGKABAH01 5', mRNA sequence.
ACCESSION AV717947
VERSION AV717947.2 GI:37804993
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 262)
AUTHORS Xiao.H., Xu.X., Li.N., Peng.Y., Liu.F., Qu.J., Song.H., Cheng.Z.,
Zeng.L., Xu.S., Gu.W., Tu.Y., Jia.J., Fu.G., Ren.S., Zhong.M.,
Lu.G., Yang.Y., Gu.Y., Chen.Z. and Han,Z.
LAB_HOST="GK"
LAB_LIB="GK"
TITLE Homo sapiens cDNA GK clones
JOURNAL Unpublished (2000)
COMMENT On Oct 16, 2000 this sequence version replaced gi:10815099.
Contact: Zeguang Han
Chinese National Human Genome Center at Shanghai
351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
201203, P. R. China
Tel: 86-21-50801919 (ex.45)
Fax: 86-21-50801922
Email: hanzgchgc.sh.cn
This clone is available at CHGC in Shanghai.
FEATURES
source
Location/Qualifiers
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/organism="Homo sapiens"
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/clone="FGKABAH01"
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/dev_stage="Adult"
/lab_host="GK"
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/notes="Vector: pBluescript sk(-); Site_1: EcoRI; Site_2: XhoI"
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Query Match 5.9%; Score 40; DB 9; Length 262;
Best Local Similarity 100.0%; Pred. No. 4.9;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 496 GCCTCAGTCGGTTCTCTTGGCTCAGTTACTAGTCCCAT 535
Db 262 GCCTCAGTCGGTTCTCTTGGCTCAGTTACTAGTCCCAT 223

RESULT 7
AV717948/c
LOCUS AV717948 GK Homo sapiens cDNA clone FGKABAH03 5', mRNA linear EST 21-OCT-2003
DEFINITION AV717948 GK Homo sapiens cDNA clone FGKABAH03 5', mRNA sequence.
ACCESSION AV717948
VERSION AV717948.2 GI:37804994
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 264)
AUTHORS Xiao.H., Xu.X., Li.N., Peng.Y., Liu.F., Qu.J., Song.H., Cheng.Z.,
Zeng.L., Xu.S., Gu.W., Tu.Y., Jia.J., Fu.G., Ren.S., Zhong.M.,
Lu.G., Yang.Y., Gu.Y., Chen.Z. and Han,Z.
LAB_HOST="GK"
LAB_LIB="GK"
TITLE Homo sapiens cDNA GK clones
JOURNAL Unpublished (2000)
COMMENT On Oct 16, 2000 this sequence version replaced gi:10815100.
Contact: Zeguang Han
Chinese National Human Genome Center at Shanghai
351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
201203, P. R. China
Tel: 86-21-50801919 (ex.45)
Fax: 86-21-50801922
Email: hanzgchgc.sh.cn
This clone is available at CHGC in Shanghai.
FEATURES
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/clone="FGKABAH03"
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/dev_stage="Adult"
/lab_host="GK"
/lab_lib="GK"
/notes="Vector: pBluescript sk(-); Site_1: EcoRI; Site_2: XhoI"
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Best Local Similarity 100.0%; Pred. No. 4.9;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 496 GCCTCAGTCGGTTCTCTTGGCTCAGTTACTAGTCCCAT 535
Db 262 GCCTCAGTCGGTTCTCTTGGCTCAGTTACTAGTCCCAT 223

RESULT 8
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LOCUS AV717975 GK Homo sapiens cDNA clone FGKABAH12 5', mRNA linear EST 21-OCT-2003
DEFINITION AV717975 GK Homo sapiens cDNA clone FGKABAH12 5', mRNA sequence.
ACCESSION AV717975
VERSION AV717975.2 GI:37805020
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 268)
AUTHORS Wu.T., Qian.B., Huang.Q., Kang.B., Gao.X., Xu.Z.,
Xiao.H., Xu.X., Li.N., Peng.Y., Liu.F., Qu.J., Song.H., Cheng.Z.,
Zeng.L., Xu.S., Gu.W., Tu.Y., Jia.J., Fu.G., Ren.S., Zhong.M.,
Lu.G., Yang.Y., Gu.Y., Chen.Z. and Han,Z.
LAB_HOST="GK"
LAB_LIB="GK"
TITLE Homo sapiens cDNA GK clones
JOURNAL Unpublished (2000)
COMMENT On Oct 16, 2000 this sequence version replaced gi:10815127.
Contact: Zeguang Han
Chinese National Human Genome Center at Shanghai
351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
201203, P. R. China
Tel: 86-21-50801919 (ex.45)
Fax: 86-21-50801922
Email: hanzgchgc.sh.cn
This clone is available at CHGC in Shanghai.
FEATURES
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/organism="Homo sapiens"
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/lab_host="GK"
/lab_lib="GK"
/notes="Vector: pBluescript sk(-); Site_1: EcoRI; Site_2: XhoI"
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Best Local Similarity 100.0%; Pred. No. 4.9;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 496 GCCTCAGTCGGTTCTCTTGGCTCAGTTACTAGTCCCAT 535
Db 264 GCCTCAGTCGGTTCTCTTGGCTCAGTTACTAGTCCCAT 225

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Tel: 86-21-50801919 (ex.45)
Fax: 86-21-50801922
Email: hanzgchgc.sh.cn
This clone is available at CHGC in Shanghai.
Location/Qualifiers
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/organism="Homo sapiens"
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/clone="FGKABAH03"
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/dev_stage="Adult"
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/notes="Vector: pBluescript sk(-); Site_1: EcoRI; Site_2: XhoI"
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Query Match 5.9%; Score 40; DB 9; Length 264;
Best Local Similarity 100.0%; Pred. No. 4.9;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 496 GCCTCAGTCGGTTCTCTTGGCTCAGTTACTAGTCCCAT 535
Db 264 GCCTCAGTCGGTTCTCTTGGCTCAGTTACTAGTCCCAT 225

RESULT 8
AV717975/c
LOCUS AV717975 GK Homo sapiens cDNA clone FGKABAH12 5', mRNA linear EST 21-OCT-2003
DEFINITION AV717975 GK Homo sapiens cDNA clone FGKABAH12 5', mRNA sequence.
ACCESSION AV717975
VERSION AV717975.2 GI:37805020
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 268)
AUTHORS Wu.T., Qian.B., Huang.Q., Kang.B., Gao.X., Xu.Z.,
Xiao.H., Xu.X., Li.N., Peng.Y., Liu.F., Qu.J., Song.H., Cheng.Z.,
Zeng.L., Xu.S., Gu.W., Tu.Y., Jia.J., Fu.G., Ren.S., Zhong.M.,
Lu.G., Yang.Y., Gu.Y., Chen.Z. and Han,Z.
LAB_HOST="GK"
LAB_LIB="GK"
TITLE Homo sapiens cDNA GK clones
JOURNAL Unpublished (2000)
COMMENT On Oct 16, 2000 this sequence version replaced gi:10815127.
Contact: Zeguang Han
Chinese National Human Genome Center at Shanghai
351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
201203, P. R. China
Tel: 86-21-50801919 (ex.45)
Fax: 86-21-50801922
Email: hanzgchgc.sh.cn
This clone is available at CHGC in Shanghai.
FEATURES
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Location/Qualifiers
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/lab_lib="GK"
/notes="Vector: pBluescript sk(-); Site_1: EcoRI; Site_2: XhoI"
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Query Match 5.9%; Score 40; DB 9; Length 268;
Best Local Similarity 100.0%; Pred. No. 4.9;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 496 GCCTCAGTCGGTTCTCTTGGCTCAGTTACTAGTCCCAT 535

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Db      268 GCCTCAGTCGGTTCTCTTGGCTCAGTTTACTAGTGCCAT 229
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AV717986      269 bp      mRNA      linear      EST 21-OCT-2003
AV717986 GK Homo sapiens cDNA clone FGKABAF01 5', mRNA sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM      Homo sapiens (human)
REFERENCE
AUTHORS      Wu,T., Qian,B., Huang,Q., Kang,B., Gao,X., Xu,Z.,
Xiao,H., Xu,X., Li,N., Peng,Y., Liu,F., Qu,J., Song,H., Cheng,Z.,
Zeng,L., Xu,S., Gu,W., Tu,Y., Jia,J., Fu,G., Ren,S., Zhong,M.,
Lu,G., Yang,Y., Gu,Y., Chen,Z. and Han,Z.
Homo sapiens cDNA GK clones
Unpublished (2000)
On Oct 16, 2000 this sequence version replaced gi:10815138.
Contact: Zeguang Han
Chinese National Human Genome Center at Shanghai
351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
201203, P. R. China
Tel: 86-21-50801919(ex.45)
Fax: 86-21-50801922
Email: hanzg@chgc.sh.cn
This clone is available at CHGC in Shanghai.
FEATURES
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1..269
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/clone="FGKABAF01"
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/dev_stage="Adult"
/lab_host="SOLR"
/clone_lib="GK"
/notes="Vector: pBluescript sk(-); Site_1: EcoRI; Site_2:
XhoI"
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Query Match      5.9%; Score 40; DB 9; Length 269;
Best Local Similarity 100.0%; Pred. NO. 4.9;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY      496 GCCTCAGTCGGTTCTCTTGGCTCAGTTTACTAGTGCCAT 535
|||||
DB      269 GCCTCAGTCGGTTCTCTTGGCTCAGTTTACTAGTGCCAT 230
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RESULT 10
AV717995/c
LOCUS      AV717995 GK Homo sapiens cDNA clone FGKABAF08 5', mRNA linear      EST 21-OCT-2003
DEFINITION      AV717995
ACCESSION      AV717995
VERSION      AV717995.2 GI:37805038
KEYWORDS
SOURCE      Homo sapiens (human)
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 270)
Wu,T., Qian,B., Huang,Q., Kang,B., Gao,X., Xu,Z.,
Xiao,H., Xu,X., Li,N., Peng,Y., Liu,F., Qu,J., Song,H., Cheng,Z.,
Zeng,L., Xu,S., Gu,W., Tu,Y., Jia,J., Fu,G., Ren,S., Zhong,M.,
Lu,G., Yang,Y., Gu,Y., Chen,Z. and Han,Z.
Homo sapiens cDNA GK clones
Unpublished (2000)
On Oct 16, 2000 this sequence version replaced gi:10815147.
Contact: Zeguang Han
Chinese National Human Genome Center at Shanghai
351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
201203, P. R. China
Tel: 86-21-50801919(ex.45)
Fax: 86-21-50801922
Email: hanzg@chgc.sh.cn
This clone is available at CHGC in Shanghai.
FEATURES
source
1..269
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/mol_type="mRNA"
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/dev_stage="Adult"
/lab_host="SOLR"
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/notes="Vector: pBluescript sk(-); Site_1: EcoRI; Site_2:
XhoI"
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Query Match      5.9%; Score 40; DB 9; Length 269;
Best Local Similarity 100.0%; Pred. NO. 4.9;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY      496 GCCTCAGTCGGTTCTCTTGGCTCAGTTTACTAGTGCCAT 535
|||||
DB      269 GCCTCAGTCGGTTCTCTTGGCTCAGTTTACTAGTGCCAT 230
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RESULT 10
AV717995/c
LOCUS      AV717995 GK Homo sapiens cDNA clone FGKABAF08 5', mRNA linear      EST 21-OCT-2003
DEFINITION      AV717995
ACCESSION      AV717995
VERSION      AV717995.2 GI:37805038
KEYWORDS
SOURCE      Homo sapiens (human)
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 270)
Wu,T., Qian,B., Huang,Q., Kang,B., Gao,X., Xu,Z.,
Xiao,H., Xu,X., Li,N., Peng,Y., Liu,F., Qu,J., Song,H., Cheng,Z.,
Zeng,L., Xu,S., Gu,W., Tu,Y., Jia,J., Fu,G., Ren,S., Zhong,M.,
Lu,G., Yang,Y., Gu,Y., Chen,Z. and Han,Z.
Homo sapiens cDNA GK clones
Unpublished (2000)
On Oct 16, 2000 this sequence version replaced gi:10815147.
Contact: Zeguang Han
Chinese National Human Genome Center at Shanghai
351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
201203, P. R. China
Tel: 86-21-50801919(ex.45)
Fax: 86-21-50801922
Email: hanzg@chgc.sh.cn
This clone is available at CHGC in Shanghai.
FEATURES
source
1..270
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/dev_stage="Adult"
/lab_host="SOLR"
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/notes="Vector: pBluescript sk(-); Site_1: EcoRI; Site_2:
XhoI"
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Query Match      5.9%; Score 40; DB 9; Length 270;
Best Local Similarity 100.0%; Pred. NO. 4.9;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY      496 GCCTCAGTCGGTTCTCTTGGCTCAGTTTACTAGTGCCAT 535
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DB      270 GCCTCAGTCGGTTCTCTTGGCTCAGTTTACTAGTGCCAT 231
|||||
RESULT 11
AV718017/c
LOCUS      AV718017 GK Homo sapiens cDNA clone FGKABAE09 5', mRNA linear      EST 21-OCT-2003
DEFINITION      AV718017
ACCESSION      AV718017
VERSION      AV718017.2 GI:37805058
KEYWORDS
SOURCE      Homo sapiens (human)
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 270)
Wu,T., Qian,B., Huang,Q., Kang,B., Gao,X., Xu,Z.,
Xiao,H., Xu,X., Li,N., Peng,Y., Liu,F., Qu,J., Song,H., Cheng,Z.,
Zeng,L., Xu,S., Gu,W., Tu,Y., Jia,J., Fu,G., Ren,S., Zhong,M.,
Lu,G., Yang,Y., Gu,Y., Chen,Z. and Han,Z.
Homo sapiens cDNA GK clones
Unpublished (2000)
On Oct 16, 2000 this sequence version replaced gi:10815169.
Contact: Zeguang Han
Chinese National Human Genome Center at Shanghai
351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
201203, P. R. China
Tel: 86-21-50801919(ex.45)
Fax: 86-21-50801922
Email: hanzg@chgc.sh.cn
This clone is available at CHGC in Shanghai.
FEATURES
source
1..270
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="FGKABAE09"
/tissue_type="hepatocellular carcinoma"
/dev_stage="Adult"
/lab_host="SOLR"
/clone_lib="GK"
/notes="Vector: pBluescript sk(-); Site_1: EcoRI; Site_2:
XhoI"
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Query Match      5.9%; Score 40; DB 9; Length 270;
Best Local Similarity 100.0%; Pred. NO. 4.9;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY      496 GCCTCAGTCGGTTCTCTTGGCTCAGTTTACTAGTGCCAT 535
|||||
DB      270 GCCTCAGTCGGTTCTCTTGGCTCAGTTTACTAGTGCCAT 231
|||||

```

```

Contact: Zeguang Han
Chinese National Human Genome Center at Shanghai
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201203, P. R. China
Tel: 86-21-50801919(ex.45)
Fax: 86-21-50801922
Email: hanzg@chgc.sh.cn
This clone is available at CHGC in Shanghai.
FEATURES
source
1..270
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
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/dev_stage="Adult"
/lab_host="SOLR"
/clone_lib="GK"
/notes="Vector: pBluescript sk(-); Site_1: EcoRI; Site_2:
XhoI"
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Query Match      5.9%; Score 40; DB 9; Length 270;
Best Local Similarity 100.0%; Pred. NO. 4.9;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY      496 GCCTCAGTCGGTTCTCTTGGCTCAGTTTACTAGTGCCAT 535
|||||
DB      270 GCCTCAGTCGGTTCTCTTGGCTCAGTTTACTAGTGCCAT 231
|||||
RESULT 11
AV718017/c
LOCUS      AV718017 GK Homo sapiens cDNA clone FGKABAE09 5', mRNA linear      EST 21-OCT-2003
DEFINITION      AV718017
ACCESSION      AV718017
VERSION      AV718017.2 GI:37805058
KEYWORDS
SOURCE      Homo sapiens (human)
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 270)
Wu,T., Qian,B., Huang,Q., Kang,B., Gao,X., Xu,Z.,
Xiao,H., Xu,X., Li,N., Peng,Y., Liu,F., Qu,J., Song,H., Cheng,Z.,
Zeng,L., Xu,S., Gu,W., Tu,Y., Jia,J., Fu,G., Ren,S., Zhong,M.,
Lu,G., Yang,Y., Gu,Y., Chen,Z. and Han,Z.
Homo sapiens cDNA GK clones
Unpublished (2000)
On Oct 16, 2000 this sequence version replaced gi:10815169.
Contact: Zeguang Han
Chinese National Human Genome Center at Shanghai
351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
201203, P. R. China
Tel: 86-21-50801919(ex.45)
Fax: 86-21-50801922
Email: hanzg@chgc.sh.cn
This clone is available at CHGC in Shanghai.
FEATURES
source
1..270
/organism="Homo sapiens"
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/clone="FGKABAE09"
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/dev_stage="Adult"
/lab_host="SOLR"
/clone_lib="GK"
/notes="Vector: pBluescript sk(-); Site_1: EcoRI; Site_2:
XhoI"
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Best Local Similarity 100.0%; Pred. NO. 4.9;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY      496 GCCTCAGTCGGTTCTCTTGGCTCAGTTTACTAGTGCCAT 535
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DB      270 GCCTCAGTCGGTTCTCTTGGCTCAGTTTACTAGTGCCAT 231
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Best Local Similarity 100.0%; Pred. No. 4.9;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 496 GCCTCAGTCGCTTCTCTGCTCAGTTACTAGTGCCAT 535
Db 270 GCCTCAGTCGCTTCTCTGCTCAGTTACTAGTGCCAT 231

RESULT 12
AV717964/c
LOCUS AV717964 271 bp mRNA linear EST 21-OCT-2003
DEFINITION AV717964 GK Homo sapiens cDNA clone FKGAB08 5', mRNA sequence.
ACCESSION AV717964
VERSION AV717964.2 GI:37805010
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 271)
Xiao,H., Xu,X., Li,N., Peng,Y., Liu,F., Qu,J., Song,H., Cheng,Z.,
Zeng,L., Xu,S., Gu,W., Tu,Y., Jia,J., Fu,G., Ren,S., Zhong,M.,
Lu,G., Yang,F., Gu,Y., Chen,Z. and Han,Z.
Homo sapiens cDNA GK clones
Unpublished (2000)
On Oct 16, 2000 this sequence version replaced gi:10815116.
Contact: Zeguang Han
Chinese National Human Genome Center at Shanghai
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201203, P. R. China
Tel: 86-21-50801919(ex.45)
Fax: 86-21-50801922
Email: hanzg@chgc.sh.cn
This clone is available at CHGC in Shanghai.

FEATURES
source
1..271
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/dev_stage="Adult"
/lab_host="SOLR"
/clone_lib="GK"
/notes="Vector: pBluescript sk(-); Site_1: EcoRI; Site_2:
XhoI"

ORIGIN
Query Match 5.9%; Score 40; DB 9; Length 271;
Best Local Similarity 100.0%; Pred. No. 4.9;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 496 GCCTCAGTCGCTTCTCTGCTCAGTTACTAGTGCCAT 535
Db 271 GCCTCAGTCGCTTCTCTGCTCAGTTACTAGTGCCAT 232

RESULT 13
AV717969/c
LOCUS AV717969 300 bp mRNA linear EST 21-OCT-2003
DEFINITION AV717969 GK Homo sapiens cDNA clone FKGAB04 5', mRNA sequence.
ACCESSION AV717969
VERSION AV717969.2 GI:37805015
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 300)
Xiao,H., Xu,X., Li,N., Peng,Y., Liu,F., Qu,J., Song,H., Cheng,Z.,
Zeng,L., Xu,S., Gu,W., Tu,Y., Jia,J., Fu,G., Ren,S., Zhong,M.,
Lu,G., Yang,F., Gu,Y., Chen,Z. and Han,Z.
Homo sapiens cDNA GK clones
Unpublished (2000)
On Oct 16, 2000 this sequence version replaced gi:10815116.
Contact: Zeguang Han
Chinese National Human Genome Center at Shanghai
351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
201203, P. R. China
Tel: 86-21-50801919(ex.45)
Fax: 86-21-50801922
Email: hanzg@chgc.sh.cn
This clone is available at CHGC in Shanghai.

FEATURES
source
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/clone_lib="GK"
/notes="Vector: pBluescript sk(-); Site_1: EcoRI; Site_2:
XhoI"

ORIGIN
Query Match 5.9%; Score 40; DB 9; Length 271;
Best Local Similarity 100.0%; Pred. No. 4.9;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 496 GCCTCAGTCGCTTCTCTGCTCAGTTACTAGTGCCAT 535
Db 271 GCCTCAGTCGCTTCTCTGCTCAGTTACTAGTGCCAT 232

RESULT 14
AV718014/c
LOCUS AV718014 301 bp mRNA linear EST 21-OCT-2003
DEFINITION AV718014 GK Homo sapiens cDNA clone FKGABAF12 5', mRNA sequence.
ACCESSION AV718014
VERSION AV718014.2 GI:37805056
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 301)
Wu,T., Qian,B., Huang,Q., Huang,C., Kang,B., Gao,X., Xu,Z.,
Xiao,H., Xu,X., Li,N., Peng,Y., Liu,F., Qu,J., Song,H., Cheng,Z.,
Zeng,L., Xu,S., Gu,W., Tu,Y., Jia,J., Fu,G., Ren,S., Zhong,M.,
Lu,G., Yang,F., Gu,Y., Chen,Z. and Han,Z.
Homo sapiens cDNA GK clones
Unpublished (2000)
On Oct 16, 2000 this sequence version replaced gi:10815166.
Contact: Zeguang Han
Chinese National Human Genome Center at Shanghai
351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
201203, P. R. China
Tel: 86-21-50801919(ex.45)
Fax: 86-21-50801922
Email: hanzg@chgc.sh.cn
This clone is available at CHGC in Shanghai.

FEATURES
source
1..301
/organism="Homo sapiens"
/mol_type="mRNA"
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/dev_stage="Adult"
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/clone_lib="GK"
/notes="Vector: pBluescript sk(-); Site_1: EcoRI; Site_2:
XhoI"

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Best Local Similarity 100.0%; Pred. No. 5.1;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 496 GCCTCAGTCGCTTCTCTGCTCAGTTACTAGTGCCAT 535
Db 300 GCCTCAGTCGCTTCTCTGCTCAGTTACTAGTGCCAT 261

RESULT 15
AV718014/c
LOCUS AV718014 301 bp mRNA linear EST 21-OCT-2003
DEFINITION AV718014 GK Homo sapiens cDNA clone FKGABAF12 5', mRNA sequence.
ACCESSION AV718014
VERSION AV718014.2 GI:37805056
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 301)
Wu,T., Qian,B., Huang,Q., Huang,C., Kang,B., Gao,X., Xu,Z.,
Xiao,H., Xu,X., Li,N., Peng,Y., Liu,F., Qu,J., Song,H., Cheng,Z.,
Zeng,L., Xu,S., Gu,W., Tu,Y., Jia,J., Fu,G., Ren,S., Zhong,M.,
Lu,G., Yang,F., Gu,Y., Chen,Z. and Han,Z.
Homo sapiens cDNA GK clones
Unpublished (2000)
On Oct 16, 2000 this sequence version replaced gi:10815166.
Contact: Zeguang Han
Chinese National Human Genome Center at Shanghai
351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
201203, P. R. China
Tel: 86-21-50801919(ex.45)
Fax: 86-21-50801922
Email: hanzg@chgc.sh.cn
This clone is available at CHGC in Shanghai.

FEATURES
source
1..301
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="FGKABAF12"
/tissue_type="hepatocellular carcinoma"
/dev_stage="Adult"
/lab_host="SOLR"
/clone_lib="GK"
/notes="Vector: pBluescript sk(-); Site_1: EcoRI; Site_2:
XhoI"

ORIGIN
Query Match 5.9%; Score 40; DB 9; Length 300;
Best Local Similarity 100.0%; Pred. No. 5.1;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 496 GCCTCAGTCGCTTCTCTGCTCAGTTACTAGTGCCAT 535
Db 300 GCCTCAGTCGCTTCTCTGCTCAGTTACTAGTGCCAT 261

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Lu,G., Yang,Y., Gu,Y., Chen,Z. and Han,Z.
Homo sapiens cDNA GK clones
Unpublished (2000)
On Oct 16, 2000 this sequence version replaced gi:10815121.
Contact: Zeguang Han
Chinese National Human Genome Center at Shanghai
351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
201203, P. R. China
Tel: 86-21-50801919(ex.45)
Fax: 86-21-50801922
Email: hanzg@chgc.sh.cn
This clone is available at CHGC in Shanghai.

FEATURES
source
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/clone_lib="GK"
/notes="Vector: pBluescript sk(-); Site_1: EcoRI; Site_2:
XhoI"

ORIGIN
Query Match 5.9%; Score 40; DB 9; Length 300;
Best Local Similarity 100.0%; Pred. No. 5.1;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 496 GCCTCAGTCGCTTCTCTGCTCAGTTACTAGTGCCAT 535
Db 300 GCCTCAGTCGCTTCTCTGCTCAGTTACTAGTGCCAT 261

RESULT 16
AV718014/c
LOCUS AV718014 301 bp mRNA linear EST 21-OCT-2003
DEFINITION AV718014 GK Homo sapiens cDNA clone FKGABAF12 5', mRNA sequence.
ACCESSION AV718014
VERSION AV718014.2 GI:37805056
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 301)
Wu,T., Qian,B., Huang,Q., Huang,C., Kang,B., Gao,X., Xu,Z.,
Xiao,H., Xu,X., Li,N., Peng,Y., Liu,F., Qu,J., Song,H., Cheng,Z.,
Zeng,L., Xu,S., Gu,W., Tu,Y., Jia,J., Fu,G., Ren,S., Zhong,M.,
Lu,G., Yang,F., Gu,Y., Chen,Z. and Han,Z.
Homo sapiens cDNA GK clones
Unpublished (2000)
On Oct 16, 2000 this sequence version replaced gi:10815166.
Contact: Zeguang Han
Chinese National Human Genome Center at Shanghai
351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
201203, P. R. China
Tel: 86-21-50801919(ex.45)
Fax: 86-21-50801922
Email: hanzg@chgc.sh.cn
This clone is available at CHGC in Shanghai.

FEATURES
source
1..301
/organism="Homo sapiens"
/mol_type="mRNA"
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/dev_stage="Adult"
/lab_host="SOLR"
/clone_lib="GK"
/notes="Vector: pBluescript sk(-); Site_1: EcoRI; Site_2:
XhoI"

ORIGIN
Query Match 5.9%; Score 40; DB 9; Length 300;
Best Local Similarity 100.0%; Pred. No. 5.1;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 496 GCCTCAGTCGCTTCTCTGCTCAGTTACTAGTGCCAT 535
Db 300 GCCTCAGTCGCTTCTCTGCTCAGTTACTAGTGCCAT 261

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XhoI"

ORIGIN

Query Match 5.9%; Score 40; DB 9; Length 301;
Best Local Similarity 100.0%; Pred. No. 5.1;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 496 GCCTCAGTCGGTTCTCTGGCTCAGTTACTAGTGCCAT 535
|||
Db 301 GCCTCAGTCGGTTCTCTGGCTCAGTTACTAGTGCCAT 262

RESULT 15

AV718019/c
LOCUS AV718019 GK Homo sapiens cDNA clone FGAABC02 5', mRNA linear EST 21-OCT-2003
DEFINITION AV718019
ACCESSION AV718019
VERSION AV718019.2 GI:37805060
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 301)
Wu, T., Qian, B., Huang, Q., Kang, B., Gao, X., Xu, Z.,
Xiao, H., Xu, X., Li, N., Peng, Y., Liu, F., Qu, J., Song, H., Cheng, Z.,
Zeng, L., Xu, S., Gu, W., Tu, Y., Jia, J., Fu, G., Ren, S., Zhong, M.,
Lu, G., Yang, Y., Gu, Y., Chen, Z. and Han, Z.

TITLE Homo sapiens cDNA GK clones
JOURNAL Unpublished (2000)
COMMENT On Oct 16, 2000 this sequence version replaced gi:10815171.
Contact: Zeguang Han
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351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
201203, P. R. China
Tel: 86-21-50801919 (ex.45)
Fax: 86-21-50801922
Email: hanzg@chgc.sh.cn
This clone is available at CHGC in Shanghai.

FEATURES

Source
1..301
Location/Qualifiers
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/db_xref="taxon:9606"
/clone="FGKABC02"
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/dev_stage="Adult"
/lab_host="SOLR"
/clone_lib="GK"
/notes="Vector: pBluescript sk(-); Site_1: EcoRI; Site_2:
XhoI"

ORIGIN

Query Match 5.9%; Score 40; DB 9; Length 301;
Best Local Similarity 100.0%; Pred. No. 5.1;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 496 GCCTCAGTCGGTTCTCTGGCTCAGTTACTAGTGCCAT 535
|||
Db 301 GCCTCAGTCGGTTCTCTGGCTCAGTTACTAGTGCCAT 262

Search completed: July 26, 2004, 15:25:24
Job time : 2413 secs

